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OM nucleic - nucleic search, using sw model

Run on: March 18, 2005, 06:59:55 ; Search time 2319 Seconds

(without alignments)
9319.114 Million cell updates/sec

Title: US-09-763-019-5

Perfect score: 446

Sequence: 1 atgggtgaatcggtcggtgc.....ttccaaacgtgaacatccg 446

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
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4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
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9: gb.pr.*
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12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	446	100.0	446	6	BD223232
2	446	100.0	446	6	BD240919
3	287.2	64.4	606	6	BD223236
4	284	63.7	557	6	BD223246
5	215.2	48.3	534	6	BD223234
6	215.2	48.3	534	6	BD240936
7	212	47.5	485	6	BD223245
8	177.2	39.7	577	6	BD240918
9	173.2	38.8	485	6	BD223243
10	172.2	38.6	446	6	BD223239
11	170	38.1	1093	6	BD223244
12	169.2	37.9	522	6	BD223233
13	168.6	37.8	460	6	AX046745
14	168.6	37.8	503	6	AX046743
15	167.2	37.5	534	6	BD223237
16	166	37.2	434	6	BD223242
17	166	37.2	437	6	BD223241
18	166	37.2	443	6	BD223240
19	166	37.2	488	6	BD223248

20	166	37.2	575	6	BD223249	Method of
21	165.6	37.1	316	6	BD223238	BD223238
22	165.6	37.1	316	6	BD240937	BD240937
23	164	36.8	485	6	BD223247	BD223247
24	157.8	35.4	523	6	BD240916	BD240916
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37	134.4	30.1	385	6	BD240917	BD240917
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42	99.4	22.3	150	6	AR130262	AR130262
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ALIGNMENTS

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LOCUS	BD223232	Method of genetic expression of polyprotein in plant.			
DEFINITION	BD223232	Method of genetic expression of polyprotein in plant.			
ACCESSION	BD223232				
VERSION	BD223232.1	GI:33033002			
KEYWORDS	JP 2002523047-A/1.				
SOURCE	Dahlia merckii (bedding dahlia)				
ORGANISM	Dahlia merckii				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Coreopsiadeae; Dahlia.				
AUTHORS	1 (bases 1 to 446) Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.				
TITLE	Method of genetic expression of polyprotein in plant				
JOURNAL	Patent: JP 2002523047-A 1 30-JUL-2002;				
COMMENT	SYNGENTA LTD				
	OS Dahlia merckii				
	PN JP 2002523047-A/1				
	PD 30-JUL-2002				
	PF 17-AUG-1999 JP 2000566429				
	PR 18-AUG-1998 GB 9818001.1,04-DEC-1998 GB 9826753.7 PI				
	WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE				
	AUGUSTINE FRANCOIS,				
	PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI				
	ANTHONY RAY				
	PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02, C12N5/10, PC				
	C12R1:911,				
	PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)				
	CC Method of genetic expression of polyprotein in plant FH Key				
	Location/Qualifiers				
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Best Local Similarity 100.0%; Pred. No. 7.4e-105;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
BD240919

LOCUS BD240919 446 bp DNA linear PAT 17-JUL-2003
DEFINITION Polynucleotide sequences.
ACCESSION BD240919
VERSION BD240919.1 GI:33050689
KEYWORDS Dahlia merckii (bedding dahlia)
SOURCE Dahlia merckii
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Coreopsidae; Dahlia.
REFERENCE 1 (bases 1 to 446)
AUTHORS Evans, I.J. and Ray, J.A.
TITLE Polynucleotide sequences
JOURNAL Patent: JP 2002523052-A 5 30-JUL-2002;
COMMENT SYNGENTA LTD
OS Dahlia merckii (dahlia)
PN JP 2002523052-A/5
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566448
PR 18-AUG-1998 GB 9818003.7
PI IAN JEFFREY EVANS,JOHN ANTHONY RAY
PC C12N15/09,A01H5/00,C07K14/415,C12N5/10/(C12N5/10,C12R1:91),
PC C12N15/00,
CC Polynucleotide sequences
CDS Location/Qualifiers
FH Key Location/Qualifiers
FT CDS (1)..(64)
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Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGTGAATCGGTGGTTCCTTCGCGGTTCGTTCTGATCCCTTTTCGTCGCGCATC 60

QY 61 TCAGGTTATCAAACTCTTTCGTTTCATTTATGAAATAGATAGTATTTATTTATG 120
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QY 361 AAGCGGAAAGCTGCTCAAGACAACTTAATGCGCAAAAGCTTGACCGTATGCCAAGA 420
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QY 421 AAGTGGTTCCTCAAGCTTGAACATCCG 446
DB 421 AAGTGGTTCCTCAAGCTTGAACATCCG 446

RESULT 3
BD223236

LOCUS BD223236 606 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of genetic expression of polyprotein in plant.
ACCESSION BD223236
VERSION BD223236.1 GI:33033006
KEYWORDS JP 2002523047-A/5.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 606)
AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.
TITLE Method of genetic expression of polyprotein in plant
JOURNAL Patent: JP 2002523047-A 5 30-JUL-2002;
COMMENT SYNGENTA LTD
OS Artificial Sequence
PN JP 2002523047-A/5
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1,04-DEC-1998 GB 9826753.7 PI
PI WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
PI AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI ANTHONY RAY
PC C12N15/09,A01H1/00,C07K12,C12N5/10,C12P21/02/(C12N5/10, PC C12R1:91),
PC C12N15/00,C12N5/00,(C12N5/00,C12R1:91)
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RESULT 6
LOCUS BD240936
DEFINITION Polynucleotide sequences.
ACCESSION BD240936
VERSION BD240936.1 GI:33050706
KEYWORDS JP 2002523052-A/22.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 534)
AUTHORS Evans, I.J. and Ray, J.A.
TITLE Polynucleotide sequences
JOURNAL SYNGENTA LTD
COMMENT OS Artificial Sequence
PN JP 2002523052-A/22
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566448
PR 18-AUG-1998 GB 9818003.7
PI IAN JEFFREY EVANS, JOHN ANTHONY RAY
PC C12N15/00,
PC C12N15/00, (C12N5/00, C12R1:91)
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Key CDS Location/Qualifiers
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Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 155 AGATATCGCATCGGTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
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QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGGAGGTGCGGCCCATGG 274
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QY 335 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGAAACAATC 374
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RESULT 7
LOCUS BD223245
DEFINITION Method of genetic expression of polypeptide in plant.
ACCESSION BD223245
VERSION BD223245.1 GI:33033015
KEYWORDS JP 2002523047-A/14.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 485)
AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.

QY 335 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGAAACAATC 374
Db 318 CGAAAAGCTTGCTCAAGACAACTTAAAGCCGAAACAATC 357

RESULT 8
LOCUS BD240918
DEFINITION Polynucleotide sequences.
ACCESSION BD240918
VERSION BD240918.1 GI:33050688
KEYWORDS JP 2002523052-A/4.
SOURCE Dahlia merckii (bedding dahlia)
ORGANISM Dahlia merckii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Coreopsiodeae; Dahlia.
REFERENCE 1 (bases 1 to 577)
AUTHORS Evans, I.J. and Ray, J.A.
TITLE Polynucleotide sequences
JOURNAL Patent: JP 2002523052-A 4 30-JUL-2002; SYNGENTA LTD
COMMENT OS Dahlia merckii (dahlia)
PN JP 2002523052-A/4
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566448
PR 18-AUG-1998 GB 9818003.7
PI IAN JEFFREY EVANS, JOHN ANTHONY RAY
PC C12N15/09, A01H5/00, C07K14/415, C12N5/10, (C12N5/10, C12R1:91),
PC C12N5/00,
PC C12N5/00, (C12N5/00, C12R1:91)

TITLE JOURNAL
COMMENT Method of genetic expression of polypeptide in plant
SYNGENTA LTD
OS Artificial Sequence
PN JP 2002523047-A 14 30-JUL-2002;
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/09, A01H1/00, C07K11/12, C12N5/10, C12P21/02, (C12N5/10, PC
C12R1:91),
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RESULT 8
LOCUS BD240918
DEFINITION Polynucleotide sequences.
ACCESSION BD240918
VERSION BD240918.1 GI:33050688
KEYWORDS JP 2002523052-A/4.
SOURCE Dahlia merckii (bedding dahlia)
ORGANISM Dahlia merckii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Coreopsiodeae; Dahlia.
REFERENCE 1 (bases 1 to 577)
AUTHORS Evans, I.J. and Ray, J.A.
TITLE Polynucleotide sequences
JOURNAL Patent: JP 2002523052-A 4 30-JUL-2002; SYNGENTA LTD
COMMENT OS Dahlia merckii (dahlia)
PN JP 2002523052-A/4
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566448
PR 18-AUG-1998 GB 9818003.7
PI IAN JEFFREY EVANS, JOHN ANTHONY RAY
PC C12N15/09, A01H5/00, C07K14/415, C12N5/10, (C12N5/10, C12R1:91),
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DB 262 CGAAAGCTT-----GCTCAAGACAAAGTGAATGCG 291
QY 395 CCAAGAGCTTGACCGTGTGATGCGCAAGAAAGTGTCCAAAGCTTGACATCCG 446
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RESULT 9
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DEFINITION
ACCESSION
VERSION
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AUTHORS
TITLE
JOURNAL
COMMENT
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PN JP 2002523047-A/12
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1.04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02, (C12N5/10, PC
C12R1:91),
PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)
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COMMENT
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PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1.04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02, (C12N5/10, PC
C12R1:91),
PC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)
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Query Match 38.6%; Score 172.2; DB 6; Length 446;
Best Local Similarity 93.3%; Pred. No. 7.3e-34;
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DB 65 AGATATCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGCAA 124
QY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCTACTGGAGGGGGCGGCCCATGG 274

Db 125 CTGTGGCAACGCGGACATTGTGACAAACAATGTAATCATGGAGGGTGGCGTCAAGG 184
QY 275 AGCGTGTGATGCTGCTAAGCGGACACATGTTCTGTTACTTCAATTGTAAGG 334
Db 185 AGCGTGTGATGCTGCTAAGCGGACACATGTTCTGTTACTTCAATTGTAAGGCGG 244
QY 335 CGAAAGCTTCTGCT 347
Db 245 CGACGAGTGGCT 257

RESULT 11
LOCUS BD223244 1093 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of genetic expression of polyprotein in plant.
ACCESSION BD223244
VERSION BD223244.1 GI:33033014
KEYWORDS JP 2002523047-A/13.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1093)
AUTHORS Broekaert,W.F., Francois,I.E.J.A., Bolle,M.F.C.D., Evans,I.J. and Ray,J.A.
TITLE Method of genetic expression of polyprotein in plant
JOURNAL SINGENTA LTD
COMMENT OS Artificial Sequence
PN JP 2002523047-A/13
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1,04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/00,A01H1/00,C07K1/12,C12N5/10,C12P21/02//(C12N5/10, PC
C12R1:91),
PC C12N15/00,C12N5/00,(C12N5/00,C12R1:91)
CC Description of Artificial Sequence: Synthetic sequence FH
Key CDS Location/Qualifiers
FT CDS (3)..(1085).

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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 84.3%; Pred. No. 2.8e-33;
Matches 204; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGCATGGTCGGGAAA 214
Db 65 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGCATGGTCGGGCAA 124
QY 215 CTGTGGCAATACGGGACATTTGACCAACCAATGTAATCATGGAGGGTGGCGCCATGG 274
Db 125 CTGTGGCAACACGGGACATTTGACCAACCAATGTAATCATGGAGGGTGGCGGTCACGG 184
QY 275 AGCGTGTGATGCTGCTAAGCGGAAACACATGTTTCTGTTACTTCAATTGTAAGG 334
Db 185 AGCGTGTGATGCTGCTAAGCGGAAACACATGTTTCTGTTACTTCAACTGCGCTAACGC 244
QY 335 CGAAAGCTTCTCAAGCAAACTTAAG---CCGAACAACCTGCTCAAGCAAACTTAA 391
Db 245 TGAGGAAGCTGCTGCTGCTATTCTTGAAGCTTCTGAAGAACTTGCTCAAGAAAGCTCC 304
QY 392 TG 393
Db 305 TG 306

RESULT 12
LOCUS BD223233
DEFINITION Method of genetic expression of polyprotein in plant.
ACCESSION BD223233
VERSION BD223233.1 GI:33033003
KEYWORDS JP 2002523047-A/2.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 522)
AUTHORS Broekaert,W.F., Francois,I.E.J.A., Bolle,M.F.C.D., Evans,I.J. and Ray,J.A.
TITLE Method of genetic expression of polyprotein in plant
JOURNAL SINGENTA LTD
COMMENT OS Artificial Sequence
PN JP 2002523047-A/2
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1,04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/09,A01H1/00,C07K1/12,C12N5/10,C12P21/02//(C12N5/10, PC
C12R1:91),
PC C12N15/00,C12N5/00,(C12N5/00,C12R1:91)
CC Description of Artificial Sequence: Synthetic sequence FH
Key CDS Location/Qualifiers
FT CDS (76)..(513).

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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 95.6%; Pred. No. 4.4e-33;
Matches 174; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGCATGGTCGGGAAA 214
Db 138 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGCATGGTCGGGCAA 197
QY 215 CTGTGGCAATACGGGACATTTGACCAACCAATGTAATCATGGAGGGTGGCGCCATGG 274
Db 198 CTGTGGCAACACGGGACATTTGACCAACCAATGTAATCATGGAGGGTGGCGCCATGG 257
QY 275 AGCGTGTGATGCTGCTAAGCGGAAACACATGTTTCTGTTACTTCAATTGTAAGG 334
Db 258 AGCGTGTGATGCTGCTAAGCGGAAACACATGTTTCTGTTACTTCAATTGTTCCAACGC 317
QY 335 CG 336
Db 318 TG 319

RESULT 13
LOCUS AX046745 460 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 3 from Patent WO0068405.
ACCESSION AX046745
VERSION AX046745.1 GI:11876281
KEYWORDS Dimorphanthea sinuata (African daisy)
SOURCE Dimorphanthea sinuata
ORGANISM Dimorphanthea sinuata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteraceae;
Calenduleae; Dimorphanthea.

Query Match 38.1%; Score 170; DB 6; Length 1093;
Best Local Similarity 84.3%; Pred. No. 2.8e-33;
Matches 204; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGCATGGTCGGGAAA 214
Db 65 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGCATGGTCGGGCAA 124
QY 215 CTGTGGCAATACGGGACATTTGACCAACCAATGTAATCATGGAGGGTGGCGCCATGG 274
Db 125 CTGTGGCAACACGGGACATTTGACCAACCAATGTAATCATGGAGGGTGGCGGTCACGG 184
QY 275 AGCGTGTGATGCTGCTAAGCGGAAACACATGTTTCTGTTACTTCAATTGTAAGG 334
Db 185 AGCGTGTGATGCTGCTAAGCGGAAACACATGTTTCTGTTACTTCAACTGCGCTAACGC 244
QY 335 CGAAAGCTTCTCAAGCAAACTTAAG---CCGAACAACCTGCTCAAGCAAACTTAA 391
Db 245 TGAGGAAGCTGCTGCTGCTATTCTTGAAGCTTCTGAAGAACTTGCTCAAGAAAGCTCC 304
QY 392 TG 393
Db 305 TG 306

RESULT 13
LOCUS AX046745 460 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 3 from Patent WO0068405.
ACCESSION AX046745
VERSION AX046745.1 GI:11876281
KEYWORDS Dimorphanthea sinuata (African daisy)
SOURCE Dimorphanthea sinuata
ORGANISM Dimorphanthea sinuata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteraceae;
Calenduleae; Dimorphanthea.

Query Match 38.1%; Score 170; DB 6; Length 1093;
Best Local Similarity 84.3%; Pred. No. 2.8e-33;
Matches 204; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGCATGGTCGGGAAA 214
Db 65 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGCATGGTCGGGCAA 124
QY 215 CTGTGGCAATACGGGACATTTGACCAACCAATGTAATCATGGAGGGTGGCGCCATGG 274
Db 125 CTGTGGCAACACGGGACATTTGACCAACCAATGTAATCATGGAGGGTGGCGGTCACGG 184
QY 275 AGCGTGTGATGCTGCTAAGCGGAAACACATGTTTCTGTTACTTCAATTGTAAGG 334
Db 185 AGCGTGTGATGCTGCTAAGCGGAAACACATGTTTCTGTTACTTCAACTGCGCTAACGC 244
QY 335 CGAAAGCTTCTCAAGCAAACTTAAG---CCGAACAACCTGCTCAAGCAAACTTAA 391
Db 245 TGAGGAAGCTGCTGCTGCTATTCTTGAAGCTTCTGAAGAACTTGCTCAAGAAAGCTCC 304
QY 392 TG 393
Db 305 TG 306

REFERENCE 1
AUTHORS Miao,G.H., Weng,Z. and Famodu,O.O.
TITLE Plant defensins
JOURNAL Patent: WO 0068405-A 3 16-NOV-2000;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:112408"
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Best Local Similarity 81.6%; Pred. No. 6.3e-33;
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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DB 87 AGAATCGGACTGTGTGAGAAAGTCACTATGTGAGAAAGCTAGCAAGACATGTCAGGCAA 146
QY 215 CTGTGGCAATACGGACATTTGTGACACCAATGTAATCATGGAGGGTGGGCCCATGG 274
DB 147 CTGTGGCAACACGGACACTGTGACGACCACTGTAAGTGTGAGAGACTGCAGGCCCATGG 206
QY 275 ACGGTGTATGTCGTAAACGGGAAACACATGTTCTGTACTTCAATTGTAAGAAAGC 334
DB 207 TCGGTGTATGTCGTGAGGAAACACATGTCGTACTTCAATTGTAAGAAAGC 266
QY 335 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAAACACTCGCTCAAGCAAACTTAAATG 393
DB 267 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAAACACTCGCTCAAGCAAACTTAAATG 325
RESULT 14
AX046743
LOCUS AX046743 503 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 1 from Patent WO0068405.
ACCESSION AX046743
VERSION AX046743.1 GI:11876280
KEYWORDS Dimorphotheca sinuata (African daisy)
SOURCE Dimorphotheca sinuata
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Calenduleae; Dimorphotheca.
REFERENCE 1
AUTHORS Miao,G.H., Weng,Z. and Famodu,O.O.
TITLE Plant defensins
JOURNAL Patent: WO 0068405-A 1 16-NOV-2000;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
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1. 503
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Query Match 37.8%; Score 168.6; DB 6; Length 503;
Best Local Similarity 81.6%; Pred. No. 6.3e-33;
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCCAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 80 AGAATCGGACTGTGTGAGAAAGTCACTATGTGAGAAAGCTAGCAAGACATGTCAGGCAA 139

QY 215 CTGTGGCAATACGGGACATTTGTGACACCAATGTAATCATGCGGGGTGGGCCCATGG 274
DB 140 CTGTGGCAACACGGGACACTGTGTGACGACCACTGTAAGTCTGGGAGACTGCAGGCCCATGG 199
QY 275 ACGGTGTATGTCGTAAACGGGAAACACATGTTCTGTACTTCAATTGTAAGAAAGC 334
DB 200 TCGGTGTATGTCGTGAGGAAACACATGTTCTGTACTTCAATTGTAAGAAAGC 259
QY 335 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAAACACTCGCTCAAGCAAACTTAAATG 393
DB 260 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAAACACTCGCTCAAGCAAACTTAAATG 318
RESULT 15
BD223237
LOCUS BD223237 534 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of genetic expression of polyprotein in plant.
ACCESSION BD223237
VERSION BD223237.1 GI:33033007
KEYWORDS JP 2002523047-A/6.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 534)
AUTHORS Broekaert,W.F., Francois,I.E.J.A., Bolle,M.F.C.D., Evans,I.J. and Ray,J.A.
TITLE Method of genetic expression of polyprotein in plant
JOURNAL Patent: JP 2002523047-A 6 30-JUL-2002;
SYNGENTA LTD
COMMENT OS Artificial Sequence
PN JP 2002523047-A/6
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1.04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/09,A01H1/00,C07K1/12,C12N5/10,C12P21/02//C12N5/10, PC
C12R1:91),
PC C12N15/00,C12N5/00,(C12N5/00,C12R1:91)
CC Description of Artificial Sequence: Synthetic sequence FH
Key Location/Qualifiers
FT CDS (76)..(525).
FEATURES
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 98.3%; Pred. No. 1.5e-32;
Matches 169; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 138 AGATATCGCATCCGTTAGTGGAGAACTATGCCAGAAAGCTAGCAAGACATGTCGGGCAA 197
QY 215 CTGTGGCAATACGGGACATTTGTGACACCAATGTAATCATGCGGGGTGGGCCCATGG 274
DB 198 CTGTGGCAACACGGGACATTTGTGACACCAATGTAATCATGCGGGGTGGGCCCATGG 257
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DB 258 ACGGTGTATGTCGTAAACGGGAAACACATGTTCTGTACTTCAATTGT 309
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Job time : 2320 secs

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GenCore version 5.1.6
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Run on: March 18, 2005, 06:45:35 ; Search time 388 Seconds
(without alignment)
6804.651 Million cell updates/sec

Title: US-09-763-019-5
Perfect score: 446
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001s:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	446	100.0	446	Aaz51379	Dahlia me
2	446	100.0	446	Aaz99331	DNA encod
3	287.2	64.4	606	Aaz99336	DNA encod
4	284	63.7	557	Aaz99336	DNA encod
5	215.2	48.3	534	Aaz51396	Portion o
6	215.2	48.3	534	Aaz99325	DNA encod
7	212	47.5	485	Aaz99335	DNA encod
8	209.4	47.0	529	Adm77231	Ironweed
9	203	45.5	579	Adm77214	Ironweed
10	177.2	39.7	577	Aaz51378	Dahlia me
11	173.2	38.8	485	Aaz99333	DNA encod
12	172.2	38.6	446	Aaz99329	DNA encod
13	170	38.1	1093	Aaz99334	DNA encod
14	169.2	37.9	522	Aaz99324	DNA encod
15	168.6	37.8	460	Aaz54387	DNA encod
16	168.6	37.8	460	Adm77186	African d
17	168.6	37.8	503	Aaz54386	Plant def
18	168.6	37.8	503	Adm77184	African d
19	167.2	37.5	534	Aaz99327	DNA encod
20	166	37.2	434	Aaz99332	DNA encod

21	166	37.2	437	3	Aaz99331	DNA encod
22	166	37.2	443	3	Aaz99330	DNA encod
23	166	37.2	488	3	Aaz99338	DNA encod
24	166	37.2	575	3	Aaz99339	DNA encod
25	165.6	37.1	316	3	Aaz51397	Portion o
26	165.6	37.1	316	3	Aaz99328	DNA of pf
27	164	36.8	485	3	Aaz99337	DNA encod
28	161	36.1	461	11	Adm77229	Sunflower
29	157.8	35.4	523	3	Aaz51376	Dahlia me
30	156.4	35.1	457	5	Aaz54392	Plant def
31	156.4	35.1	457	11	Adm77196	Mexican r
32	156.4	35.1	463	5	Aaz54390	Plant def
33	156.4	35.1	463	11	Adm77192	Mexican r
34	156.4	35.1	603	5	Aaz54391	Plant def
35	156.4	35.1	603	11	Adm77194	Mexican r
36	154.8	34.7	458	5	Aaz54396	Plant def
37	154.8	34.7	458	11	Adm77204	Mexican r
38	154.8	34.7	460	5	Aaz54394	Plant def
39	154.8	34.7	460	11	Adm77200	Mexican r
40	154.2	34.6	565	5	Aaz84841	Sunflower
41	153.2	34.3	464	5	Aaz54395	Plant def
42	153.2	34.3	464	11	Adm77202	Mexican r
43	153.2	34.3	472	5	Aaz54397	Plant def
44	153.2	34.3	472	11	Adm77206	Mexican r
45	146.8	32.9	399	3	Aaz51375	Dahlia me

ALIGNMENTS

RESULT 1
Aaz51379
ID Aaz51379 standard; DNA; 446 BP.

AC Aaz51379;

DT 06-JUN-2000 (first entry)

DE Dahlia merckii antimicrobial protein Dm-AMPI gene.

KW Antimicrobial protein; Dm-AMPI; transgenic plant; microbial infection;
KW bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower;
KW apple; ds.

OS Dahlia merckii.

PH Key

FT CDS

Location/Qualifiers

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/tag= a

/product= "Antimicrobial protein Dm-AMPI"

/note= "Does not include stop codon"

/partial

1..176

FT sig_peptide

/tag= e

/note= "excludes intron"

1..64

/tag= b

/number= 1

65..156

/tag= c

/number= 1

157..446

/tag= d

/number= 2

177..326

/tag= f

/product= "Mature Dm-AMPI protein"

327..446

/tag= g

/note= "Encodes protein which may be used as cleavable linker in the co-expression of multiple proteins"

FT misc_feature

XX WO200011196-A1.

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XX PD 02-MAR-2000.
XX PF 17-AUG-1999; 99WO-GB002720.
XX PR 18-AUG-1998; 98GB-00018003.
XX (ZENE ) ZENECA LTD.
XX PA Evans IJ, Ray JA;
XX PI
XX PT WPI; 2000-237658/20.
XX DR P-PSDB; AAY70315.
XX
XX Polynucleotide sequences and expression products useful for producing
XX transgenic plants that are resistant to microbial infections.
XX
XX Claim 1; Fig 1A; 77pp; English.
XX
XX The present sequence is a Dahlia merckii cDNA encoding an antimicrobial
XX preprotein Dm-AMPI. This sequence is useful in the production of
XX transgenic plants which show improved resistance to infections by
XX microorganisms such as bacteria and fungi. Transgenic plants include e.g.
XX field crops, fruits and vegetables, such as canola, sunflower, tomato,
XX apple, banana, pear and mango
XX
XX SQ Sequence 446 BP; 128 A; 86 C; 104 G; 128 T; 0 U; 0 Other;

Query Match 100.0%; Score 446; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 9.9e-113;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGAATCGGTGGTTCCTCCGCGTTCCTCGTTCGTATCCCTTTCGTCTCGCCATC 60
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QY 61 TCAGGTTATCAATCTTTAGTTCATTTTGAATATGATAGTATTTATTTCTTTTATGG 120
Db 61 TCAGGTTATCAATCTTTAGTTCATTTTGAATATGATAGTATTTATTTCTTTTATGG 120

QY 121 TTTATGTGTTCTGCAAGTTGCAAAATTTAGTAGATATCGCATCCGTTAGTGAGAAC 180
Db 121 TTTATGTGTTCTGCAAGTTGCAAAATTTAGTAGATATCGCATCCGTTAGTGAGAAC 180

QY 181 TATGCGAAGACTAGCAAGACATGTCGCGAACTGTGGCAATACGGGACATTTGTGACA 240
Db 181 TATGCGAAGACTAGCAAGACATGTCGCGAACTGTGGCAATACGGGACATTTGTGACA 240

QY 241 ACCAATGTAATCATGGAGGGTGGCGCCCATGGAGCGTGTGATGCGTAAACGGGAAC 300
Db 241 ACCAATGTAATCATGGAGGGTGGCGCCCATGGAGCGTGTGATGCGTAAACGGGAAC 300

QY 301 ACATGTGTTTCTGTACTTCAATTGTAATAAAGCGGAAAGCTTCTCAAGACAACTTA 360
Db 301 ACATGTGTTTCTGTACTTCAATTGTAATAAAGCGGAAAGCTTCTCAAGACAACTTA 360

QY 361 AAGCGGAACAACCTGCTCAAGACAACTTAATGCCAAAGCTTCAACCGTATGCCAAGA 420
Db 361 AAGCGGAACAACCTGCTCAAGACAACTTAATGCCAAAGCTTCAACCGTATGCCAAGA 420

QY 421 AAGTGGTTCCAAACGTTGAACATCCG 446
Db 421 AAGTGGTTCCAAACGTTGAACATCCG 446
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RESULT 2

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AAZ99323
ID AAZ99323 standard; DNA; 446 BP.
XX AC AAZ99323;
XX XX
XX DT 03-JUL-2000 (first entry)
XX
```

DNA encoding the Dahlia antimicrobial protein 1 (AMPI).

Antimicrobial protein; AMPI; transgenic plant; linker propeptide; protein expression; ss.

Dahlia merckii.

Key Location/Qualifiers
CDS 1..446
/tag= a
/note= "contains 1 intron; no termination codon"
exon 1..64
/tag= b
intron 65..156
/tag= c
exon 157..446
/tag= d
mat_peptide 177..314
/tag= e

WO200011175-A1.

02-MAR-2000.

17-AUG-1999; 99WO-GB002716.

18-AUG-1998; 98GB-00018001.

04-DEC-1998; 98GB-00026753.

(ZENE) ZENECA LTD.

Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
WPI; 2000-246564/21.
P-PSDB; AAY84050.

Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.

Example 1; Fig 1; 151pp; English.

The present sequence encodes a Dahlia antimicrobial protein (AMP) 1. The AMP1 protein is used to produce transgenic plants, using the method of the invention. The specification describes methods for improving the expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence

Sequence 446 BP; 128 A; 86 C; 104 G; 128 T; 0 U; 0 Other;

Query Match 100.0%; Score 446; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 9.9e-113;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGAATCGGTGGTTCCTCCGCGTTCCTCGTTCGTATCCCTTTCGTCTCGCCATC 60
Db 1 ATGGTGAATCGGTGGTTCCTCCGCGTTCCTCGTTCGTATCCCTTTCGTCTCGCCATC 60
QY 61 TCAGGTTATCAATCTTTAGTTCATTTTGAATATGATAGTATTTATTTCTTTTATGG 120
Db 61 TCAGGTTATCAATCTTTAGTTCATTTTGAATATGATAGTATTTATTTCTTTTATGG 120
QY 121 TTTATGTGTTCTGCAAGTTGCAAAATTTAGTAGATATCGCATCCGTTAGTGAGAAC 180
121 TTTATGTGTTCTGCAAGTTGCAAAATTTAGTAGATATCGCATCCGTTAGTGAGAAC 180

[illegible]

RESULT 3
AAZ99326
ID AAZ99326 standard: DNA: 606 BP.

AC	AAZ99326;
XX	
DT	03-JUL-2000 (first entry)

DE DNA encoding a fusion protein of DmAMP1 and RSAPP2.

Antimicrobial protein; AMP1; transgenic plant; linker peptide; protein expression; plant defensin; RSP2; antifungal protein; AFP2; ss.

OS	Synthetic.
OS	Dahlia merckii.
OS	Unidentified.

AX	Key	Location/Qualifiers
FH	CDS	76..597
FT		/*tag= a
FT		160..309
FT	misc_feature	/*tag= b
FT		160..309
FT		/note="encodes DnaMP1"
FT	misc_feature	442..594
FT		/*tag= C
FT		/*tag= D

PN WO200011175-A1.

02-MAR-2000.
PD
XX

AA 17-AUG-1999: 99WO-GB002716.

AA
PR 18-AUG-1998; 98GB-00018001.

PR 04-DEC-1998; 98GB-00026753.

PA (ZENE) ZENECA LTD.

XX
PI Broekaert WF. Francois IEJA. De Bolle MFC. Evans IJ. Ray JA:

DR WPI: 2000-246564/21.

DR P-PSDB: AAY84059;

Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.

XX PS Example 2: Fig 11: 151pp; English.

XX CC The present sequence encodes a protein of the invention, comprising the

mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polypeptide is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker sequence

sequence 606 BP; 189 A; 136 C; 137 G; 144 T; 0 U; 0 Other
xx
sq

Query Match 64.4%; Score 287.2; DB 3; Length 606;
Best Local Similarity 99.0%; Pred. No. 6.1e-69;
Matches 289; Conservative 0; Mismatches 3; Indels 0

Qy	155	AGATATCGCATCCGTTAGTGGAGAACTTAGCGAGAAAGCTAGCAAGACATGTCGGGAAA	214
Db	138	AGATATCGCATCCGTTAGTGGAGAACTTAGCGAGAAAGCTAGCAAGACGTCGTCGGGCAA	197
Qy	215	CTGTGGCAATAACGGGACATTCTGACAAACCAATGTAAATCATCGGAGGGTGCGGGCCCATGG	274
Db	198	CTGTGGCAACACGGGACATTCTGACAAACCAATGTAAATCATCGGAGGGTGCGGGCCCATGG	257
Qy	275	AGCGTGTCATGTGGTGAACGGGAAACACATGTGTTTCTGTTACTTCAATGTGTAAAAAAGC	334
Db	258	AGCGTGTCATGTGGGTGAACGGGAAACACATGTGTTTCTGTTACTTCAATGTGTAAAAAAGC	317
Qy	335	CGAAAAAGCTTGCTCTCAAGACAAACTTTAAAGCCGACAAACTCGCTCAAGACAAACTTAAATGC	394
Db	318	CGAAAAAGTGTCTCAGACAAACTTTAAAGCCGACAAACTCGCTCAAGACAAACTTAAATGC	377
Qy	395	CCAAAAAGCTTGACCGTGATGCCAAGAAAGTGGTTCCTCAAAAGTTGAACATCCG	446
Db	378	CCAAAAAGCTTGACCGTGATGCCAAGAAAGTGGTTCCTCAAAAGTTGAACATCCG	429

RESULT 4
AAZ99336
ID AAZ99336 standard: DNA: 557 BP.

AA
AC
AAZ99336;

DT 03-JUL-2000 (first entry)

DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.

AA Antimicrobial protein; AMP1; transgenic plant; linker peptide;
KW protein expression; plant defensin; RAPP2; antifungal protein; AFP2; ss.
KW protein expression; plant defensin; RAPP2; antifungal protein; AFP2; ss.

XX Synthetic.

OS Dahlia merckii.

OS Unidentified.

Key	Location/Qualifiers
-----	---------------------

FT	key	production/
FT	CDS	3. .548

FT /*tag= a

FT /product= "fusion protein of DmAMP1 and RsAFP2"

PN WO200011175-A1.

02-MAR-2000.

XX 17-AUG-1999: 99WO-GB002716.

XX
PR 18-AUG-1998. 98GB-00078001

PR	18-AUG-1998;	98GB-00018001.
PR	04-DEC-1998:	98GB-00026753.

XX PA (ZENE) ZENECA LTD.

XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX DR WPI; 2000-246564/21.
XX PD P-PSDB; AAY84069.
XX
PT Improving expression of polyproteins in plants involves coexpression of
PT two or more proteins in plants within a single transcription unit.
XX PS Disclosure; Fig 31; 151pp; English.
XX
CC The present sequence encodes a protein of the invention, comprising the
CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
CC (AMP) 1 and the antifungal protein 2 (RsAFP2), linked by a linker
CC propeptide of the invention. The specification describes methods for
CC improving expression levels of one or more proteins in a transgenic
CC plant. The method comprises inserting a DNA sequence having a promoter
CC region operably linked to two or more protein encoding regions separated
CC by a DNA sequence coding for a linker propeptide and a terminator region.
CC The method is used to produce proteins in plants. The linker propeptide
CC comprising a cleavage site, whereby the expressed polypeptide is post-
CC translationally processed into the component protein molecules. The
CC propeptide sequence is rich in amino acids A, V, S and T and contains
CC dipeptidic sequences consisting of either two acidic, two basic or one
CC acidic and one basic residue as a cleavable linker sequence
XX SQ Sequence 557 BP; 164 A; 122 C; 143 G; 128 T; 0 U; 0 Other;
Query Match 63.7%; Score 284; DB 3; Length 557;
Best Local Similarity 98.3%; Pred. No. 4.5e-68;
Matches 287; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 155 AGATATCGCATCCGTTAGTGGAGAACTATCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 65 AGATATCGCATCCGTTAGTGGAGAACTATCGAGAAAGCTAGCAAGACATGTCGGGAAA 124
QY 215 CTGTGGCAATACGGGACATTTGTGACCAACAATGTTAAATCATGGGAGGTGCGGCCCATGG 274
DB 125 CTGTGGCAACACGGGACATTTGTGACCAACAATGTTAAATCATGGGAGGTGCGGCCCATGG 184
QY 275 AGCGGTGTCATGCGTAAACGGGAAACACATGTTTCTGTTACTTCAATTTGAAAAAGC 334
DB 185 AGCGGTGTCATGCGTAAACGGGAAACACATGTTTCTGTTACTTCAATTTGAAAAAGC 244
QY 335 CGAAAGCTTGTCTAAGACAACTTAAAGCCGAAACATCGCTCAAGACAACTTAAATGC 394
DB 245 CGAAAGCTTGTCTAAGACAACTTAAAGCCGAAACATCGCTCAAGACAACTTAAATGC 304
QY 395 CCAAAAGCTTGACCGTGATGCCAAGAAAGTGGTTCCAAACGTTGAACATCCG 446
DB 305 CCAAAAGCTTGACCGTGATGCCAAGAAAGTGGTTCCAAACGTTGAACATCCG 356

RESULT 5
AAZ51396
ID AAZ51396 standard; DNA; 534 BP.
AC AAZ51396;
XX
XX 06-JUN-2000 (first entry)
DT
DE Portion of pFAJ3106 encoding Dahlia merckii antimicrobial protein.
XX
XX Antimicrobial protein; DmAMP; transgenic plant; microbial infection;
KW bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower;
KW apple; plant transformation vector; ds.
XX
OS Dahlia merckii.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 76. .525
FT CDS /*tag= a
FT

FT
XX
XX WO200011196-A1.
XX PD 02-MAR-2000.
XX
XX 17-AUG-1999; 99WO-GB002720.
XX
XX 18-AUG-1998; 98GB-00018003.
XX
XX (ZENEC) ZENEC LTD.
XX
XX Evans IJ, Ray JA;
XX
XX WPI; 2000-237658/20.
XX P-PSDB; AAY70323.
XX
XX Polynucleotide sequences and expression products useful for producing
XX transgenic plants that are resistant to microbial infections.
XX
XX Example 3; Fig 7; 77pp; English.
XX
XX The present sequence corresponds to the region between XhoI and SacI
XX sites of plant transformation vector pFAJ3106, which encompasses the coding
XX region for Dahlia merckii antimicrobial protein, Dm-AMP1. The vector is
XX useful in the production of transgenic plants which show improved
XX resistance to infections by microorganisms such as bacteria and fungi.
XX Transgenic plants include e.g. field crops, fruits and vegetables, such
XX as canola, sunflower, tomato, apple, banana, pear and mango
XX
XX Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;
Query Match 48.3%; Score 215.2; DB 3; Length 534;
Best Local Similarity 98.6%; Pred. No. 4e-49;
Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 155 AGATATCGCATCCGTTAGTGGAGAACTATCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 138 AGATATCGCATCCGTTAGTGGAGAACTATCGAGAAAGCTAGCAAGACATGTCGGGAAA 197
QY 215 CTGTGGCAATACGGGACATTTGTGACCAACAATGTTAAATCATGGGAGGTGCGGCCCATGG 274
DB 198 CTGTGGCAACACGGGACATTTGTGACCAACAATGTTAAATCATGGGAGGTGCGGCCCATGG 257
QY 275 AGCGGTGTCATGCGTAAACGGGAAACACATGTTTCTGTTACTTCAATTTGAAAAAGC 334
DB 258 AGCGGTGTCATGCGTAAACGGGAAACACATGTTTCTGTTACTTCAATTTGAAAAAGC 317
QY 335 CGAAAGCTTGTCTAAGACAACTTAAAGCCGAAACATCGCTCAAGACAACTTAAATGC 374
DB 318 CGAAAGCTTGTCTAAGACAACTTAAAGCCGAAACATCGCTCAAGACAACTTAAATGC 357

RESULT 6
AAZ99325
ID AAZ99325 standard; DNA; 534 BP.
AC AAZ99325;
XX
XX 03-JUL-2000 (first entry)
DT
DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.
XX
XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
XX
OS Synthetic.
OS Dahlia merckii.
OS Unidentified.
XX
XX Key Location/Qualifiers
FH 76. .522
FT CDS /*tag= a
FT

```
FT misc_feature 160..309
FT /tag= b
FT /note= "encodes DmAMP1"
FT misc_feature 370..538
FT /tag= c
FT /note= "encodes RsAPP2"
XX
XX WO200011175-A1.
XX
XX PD 02-MAR-2000.
XX
XX PF 17-AUG-1999; 99WO-GB002716.
XX
XX PR 18-AUG-1998; 98GB-00018001.
XX PR 04-DEC-1998; 98GB-00026753.
XX
XX PA (ZENE ) ZENECA LTD.
XX
XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX
XX WPI; 2000-246564/21.
XX P-PSDB; AAY84058.
XX
XX Improving expression of polyproteins in plants involves coexpression of
XX two or more proteins in plants within a single transcription unit.
XX
XX Example 2; Fig 9; 151pp; English.
XX
XX The present sequence encodes a protein of the invention, comprising the
XX mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker
XX propeptide of the invention. The specification describes methods for
XX improving expression levels of one or more proteins in a transgenic
XX plant. The method comprises inserting a DNA sequence having a promoter
XX region operably linked to two or more protein encoding regions separated
XX by a DNA sequence coding for a linker propeptide and a terminator region.
XX The method is used to produce proteins in plants. The linker propeptide
XX translationally processed into the component protein molecules. The
XX propeptide sequence is rich in amino acids A, V, S and T and contains
XX dipeptidic sequences consisting of either two acidic, two basic or one
XX acidic and one basic residue as a cleavable linker sequence
XX
XX Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;
XX
XX Query Match 48.3%; Score 215.2; DB 3; Length 534;
XX Best Local Similarity 98.6%; Pred. No. 4e-49;
XX Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
XX |||||||
XX DB 138 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGCAA 197
XX |||||||
XX
XX QY 215 CTGTGGCAATACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCGCCCATGG 274
XX |||||||
XX DB 198 CTGTGGCAACACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCGCCCATGG 257
XX |||||||
XX
XX QY 275 AGCGTGTCATGTGCGTAAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAATAAAGC 334
XX |||||||
XX DB 258 AGCGTGTCATGTGCGTAAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAATAAAGC 317
XX |||||||
XX
XX QY 335 CGAAAAGCTTGTCTCAAGCAAACTTAAAGCCGCAACTC 374
XX |||||||
XX DB 318 CGAAAAGCTTGTCTCAAGCAAACTTAAAGCCGCAACTC 357
XX |||||||
XX
XX RESULT 7
XX AAZ99335
XX ID AAZ99335 standard; DNA; 485 BP.
XX
XX AC AAZ99335;
XX
XX DT 03-JUL-2000 (first entry)
```

XX DNA encoding a fusion protein of DmAMP1 and RsAPP2.

XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;

XX protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.

XX Synthetic.

XX Dahlia merckii.

XX Unidentified.

XX Key Location/Qualifiers

XX CDS 3..476

XX /tag= a

XX /product= "fusion protein of DmAMP1 and RsAPP2"

XX WO200011175-A1.

XX

XX PD 02-MAR-2000.

XX

XX PF 17-AUG-1999; 99WO-GB002716.

XX

XX PR 18-AUG-1998; 98GB-00018001.

XX PR 04-DEC-1998; 98GB-00026753.

XX

XX PA (ZENE) ZENECA LTD.

XX

XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX

XX WPI; 2000-246564/21.

XX P-PSDB; AAY84068.

XX

XX Improving expression of polyproteins in plants involves coexpression of

XX two or more proteins in plants within a single transcription unit.

XX

XX Disclosure; Fig 30; 151pp; English.

XX

XX The present sequence encodes a protein of the invention, comprising the

XX mature proteins of the plant defensins, the Dahlia antimicrobial protein

XX (AMP) 1 and the antifungal protein 2 (RsAPP2), linked by a linker

XX propeptide of the invention. The specification describes methods for

XX improving expression levels of one or more proteins in a transgenic

XX plant. The method comprises inserting a DNA sequence having a promoter

XX region operably linked to two or more protein encoding regions separated

XX by a DNA sequence coding for a linker propeptide and a terminator region.

XX The method is used to produce proteins in plants. The linker propeptide

XX translationally processed into the component protein molecules. The

XX propeptide sequence is rich in amino acids A, V, S and T and contains

XX dipeptidic sequences consisting of either two acidic, two basic or one

XX acidic and one basic residue as a cleavable linker sequence

XX

XX Sequence 485 BP; 139 A; 104 C; 128 G; 114 T; 0 U; 0 Other;

XX

XX Query Match 47.5%; Score 212; DB 3; Length 485;

XX Best Local Similarity 97.7%; Pred. No. 3e-48;

XX Matches 215; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

XX

XX QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214

XX |||||||

XX DB 65 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGCAA 124

XX |||||||

XX

XX QY 215 CTGTGGCAATACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCGCCCATGG 274

XX |||||||

XX DB 125 CTGTGGCAACACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCGGCTCACGG 184

XX |||||||

XX

XX QY 275 AGCGTGTCATGTGCGTAAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAATAAAGC 334

XX |||||||

XX DB 185 AGCGTGTCATGTGCGTAAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAATAAAGC 244

XX |||||||

XX

XX QY 335 CGAAAAGCTTGTCTCAAGCAAACTTAAAGCCGCAACTC 374

XX |||||||

XX DB 245 CGAAAAGCTTGTCTCAAGCAAACTTAAAGCCGCAACTC 284

XX |||||||

```
RESULT 8
ID ADM77231
XX ADM77231 standard; cDNA; 529 BP.
XX
XX
XX ADM77231;
XX
XX 03-JUN-2004 (first entry)
XX
XX Ironweed cDNA encoding mature defensin #2.
XX
XX Ironweed; ss; EST; expressed sequence tag; defensin;
XX soybean cyst nematode; pesticide; plant; plant pathogen;
XX Sclerotinia sclerotiorum; fungal infection; Candidiasis.
XX
XX Vernonia mespilifolia.
XX
XX US2003140368-A1.
XX
XX 24-JUL-2003.
XX
XX 21-JUN-2002; 2002US-00178449.
XX
XX 25-OCT-2001; 2001US-00030516.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Famodu OO, Herrmann R, Lu AL, McCutchen BF, Miao G, Presnail JK;
XX Rafaleki JA, Weng Z;
XX
XX WPI; 2003-851760/79.
XX P-PSDB; ADM77232.
XX
XX New nucleic acid molecule, useful for preparing a composition for
XX treating fungal infections, e.g. Candidiasis.
XX
XX Claim 1; SEQ ID NO 48; 69pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (either an
XX EST, expressed sequence tag or an EST contig) encoding a plant defensin
XX or its mature form, or the complement of them. Also included are a DNA
XX construct comprising the novel nucleic acid (operably linked to a
XX promoter that drives expression in a host cell), an expression cassette
XX comprising the DNA construct, a host cell having stably incorporated into
XX its genome the DNA construct, an isolated polypeptide and impacting a
XX plant pathogen e.g. soybean cyst nematode (Sclerotinia sclerotiorum). The
XX nucleic acid construct is useful for preparing a composition for treating
XX fungal infections, e.g. Candidiasis. The present sequence is either an
XX EST (expressed sequence tag) or an EST contig encoding a plant defensin
XX or its mature form.
XX
XX Sequence 529 BP; 178 A; 88 C; 111 G; 148 T; 0 U; 4 Other;
XX
XX Query Match 47.0%; Score 209.4; DB 11; Length 529;
XX Best Local Similarity 82.5%; Pred. No. 1.6e-47;
XX Matches 240; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
XX
QY 155 AGATATCCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGGTCGGGAAA 214
Db 78 AGAAATCTCGAGTGTGAGAGCAGAGCTATGCGAGAAAGCTAGCAAGACATGGTCAGGCAA 137
QY 215 CTGTGGCAATACGGGACATTTGACACCAATGTAATCATGGGAGGGTGGCGCCCATGG 274
Db 138 CTGTGGCAACACAGGACATTTGTATATCATGTGAATCATGGGAGGGTGGCGCCCATGG 197
QY 275 AGCGTGTCTATGTCGTAAACGGGAAACACATGTGTTTCTGTACTTCAATTGTAAAAAGC 334
Db 198 AGCTTGTCTATGTCGTGGAGGAAACACATGTGCTTTTGTATTTCATTTGTAAGAAAGC 257
QY 335 CGAAAGCTTCTCAAGCAACCTTAAAGCCGACAACTCGCTCAAGACAACTTAATGC 394
Db 258 TGAATAACTCGTCAAGTAAAGCTAAAGCAGAAAGCTTGTCTAAAGCAAACTCAAGGC 317

RESULT 9
ID ADM77214
XX ADM77214 standard; cDNA; 579 BP.
XX
XX ADM77214;
XX
XX 03-JUN-2004 (first entry)
XX
XX Ironweed cDNA encoding mature defensin #1.
XX
XX Ironweed; ss; EST; expressed sequence tag; defensin;
XX soybean cyst nematode; pesticide; plant; plant pathogen;
XX Sclerotinia sclerotiorum; fungal infection; Candidiasis.
XX
XX Vernonia mespilifolia.
XX
XX US2003140368-A1.
XX
XX 24-JUL-2003.
XX
XX 21-JUN-2002; 2002US-00178449.
XX
XX 25-OCT-2001; 2001US-00030516.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Famodu OO, Herrmann R, Lu AL, McCutchen BF, Miao G, Presnail JK;
XX Rafaleki JA, Weng Z;
XX
XX WPI; 2003-851760/79.
XX P-PSDB; ADM77215.
XX
XX New nucleic acid molecule, useful for preparing a composition for
XX treating fungal infections, e.g. Candidiasis.
XX
XX Claim 1; SEQ ID NO 31; 69pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (either an
XX EST, expressed sequence tag or an EST contig) encoding a plant defensin
XX or its mature form, or the complement of them. Also included are a DNA
XX construct comprising the novel nucleic acid (operably linked to a
XX promoter that drives expression in a host cell), an expression cassette
XX comprising the DNA construct, a host cell having stably incorporated into
XX its genome the DNA construct, an isolated polypeptide and impacting a
XX plant pathogen e.g. soybean cyst nematode (Sclerotinia sclerotiorum). The
XX nucleic acid construct is useful for preparing a composition for treating
XX fungal infections, e.g. Candidiasis. The present sequence is either an
XX EST (expressed sequence tag) or an EST contig encoding a plant defensin
XX or its mature form.
XX
XX Sequence 579 BP; 198 A; 97 C; 117 G; 167 T; 0 U; 0 Other;
XX
XX Query Match 45.5%; Score 203; DB 11; Length 579;
XX Best Local Similarity 81.1%; Pred. No. 9.5e-46;
XX Matches 236; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
XX
QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGGTCAGGAAA 214
Db 92 AGAAATCTCGAGTGTGAGAGCAGAGCTATGCGAGAGAGCTAGCAAGACATGGTCAGGCAA 151
QY 215 CTGTGGCAATACGGGACATTTGACACCAATGTAATCATGGGAGGGTGGCGCCCATGG 274
Db 152 CTGTGGCAACACAGGACATTTGTATAATCAGTGAATCATGGGAGGGTGGCGCCCATGG 211
QY 275 AGCGTGTCTATGTCGTGCGTAACGGGAAACACATGTGTTTCTGTACTTCAATTGTAAAAAGC 334
Db 212 AGCTTGTCTATGTCGTGGAGGAAACACATGTGCTTTTGTCTATTTCATTTGTAAAAAGC 271
```

QY 335 CGAAGAGCTTGCTCAAGCAAACTTAAAGCCGAAACAATCGCTCAAGCAAACTTAATGC 394
 Db 272 TGAAGAACTCGCTCAAGTAAGTTAAAGCTGAAGAGCTTGCAAAAGCAAACTCAAGGC 331
 QY 395 CCAAGAGCTTGACCGTGATGCGCAAGAAAGTGTTCAAACGTTGAACATCC 445
 Db 332 AGATAAGTTTGACCATGATGCAAGAGAGTAGTACCAATGTGCAACATCC 382

RESULT 10

AAZ51378

ID AAZ51378 standard; cDNA; 577 BP.

XX AAZ51378;

AC AAZ51378;

DT 06-JUN-2000 (first entry)

XX Dahlia merckii antimicrobial protein Dm2.5 cDNA.

DE Antimicrobial protein; DmAMP; Dm2.5; transgenic plant;

KW microbial infection; bacteria; fungi; field crop; fruit; vegetable;

KW canola; banana; sunflower; apple; ss.

OS Dahlia merckii.

XX

FH Key

CDS

Location/Qualifiers

20..346

/*tag= a

/product= "Antimicrobial protein Dm2.5"

/note= "Preproprotein"

20..103

sig_peptide

/*tag= b

104..253

mat_peptide

/*tag= c

/product= "Mature Dm2.5 protein"

254..343

misc_feature

/*tag= d

/note= "Encodes protein which may be used as cleavable linker in the co-expression of multiple proteins"

WO200011196-A1.

PN

02-MAR-2000.

PD

17-AUG-1999; 99WO-GB002720.

PF

18-AUG-1999; 98GB-00018003.

PR

(ZENE) ZENECA LTD.

PA

Evans IJ, Ray JA;

XX

WPI; 2000-237658/20.

DR

P-PSDB; AAY70314.

XX

Polynucleotide sequences and expression products useful for producing transgenic plants that are resistant to microbial infections.

PS Claim 1; Fig 3; 77pp; English.

XX

The present sequence is a Dahlia merckii cDNA encoding an antimicrobial preproprotein Dm2.5. This sequence is useful in the production of transgenic plants which show improved resistance to infections by microorganisms such as bacteria and fungi. Transgenic plants include e.g. field crops, fruits and vegetables, such as canola, sunflower, tomato, apple, banana, pear and mango

CC

Sequence 577 BP; 178 A; 96 C; 140 G; 163 T; 0 U; 0 Other;

SQ

Query Match

39.7%; Score 177.2; DB 3; Length 577;

Best Local Similarity

80.1%; Pred. No. 1.2e-38;

Matches 234; Conservative

0; Mismatches 28; Indels 30; Gaps 1;

1;

1;

1;

1;

1;

1;

1;

1;

QY 155 AGATATCCATCCGTTAGTGAGAACTATCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
 Db 82 AGATATCAACAAGTGTGAGAGGAGAGTATCGAGAAAGCTAGCAAGACATGTCGGGAAA 141
 QY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGCGGAGGGTGGCGCCCATGG 274
 Db 142 CTGTGGCAACACGGGACACTGTGACNACCATGTAAATCTACTGGGAGGGGGCGGCCCATGG 201
 QY 275 AGCGTGTCAATGTGCGTAACCGGAAACACATGTGTTTCTGTACTTTCAATTTGTAATAAGC 334
 Db 202 GCGGTGCCACGTCGTGGAGGAAACACATGTGTTTCTGTACTTTCAAGTGTCCCAAGC 261
 QY 335 CGAAAGCTTCTCAAGCAAACTTAAAGCCGACAACTCCGCTCAAGCAAACTTAATGC 394
 Db 262 CGAAAGCTT-----GCTCAAGCAAAAGTTAATGC 291
 QY 395 CCAAAAGCTTGACCGTGATGCCAAGAAAGTGGTCCAAACGTTGAACATCCG 446
 Db 292 CCAAGAGCTTGACCGTGATGCCAAGAAAGTGGTCCGAACTGATTCGAACTGGAACATCCG 343

RESULT 11

AAZ99333

ID AAZ99333 standard; DNA; 485 BP.

XX AAZ99333;

AC AAZ99333;

DT 03-JUL-2000 (first entry)

XX

DNA encoding a fusion protein of DmAMP1 and RsAPP2.

DE

Antimicrobial protein; AMP1; transgenic plant; linker propeptide;

KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.

KW

Synthetic.

OS Dahlia merckii.

OS Unidentified.

XX

Key

Location/Qualifiers

3..476

/*tag= a

/product= "fusion protein of DmAMP1 and RsAPP2"

WO200011175-A1.

PN

02-MAR-2000.

PD

17-AUG-1999; 99WO-GB002716.

PF

18-AUG-1998; 98GB-00018001.

PR

04-DEC-1998; 98GB-00026753.

XX

(ZENE) ZENECA LTD.

PA

Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX

WPI; 2000-246564/21.

DR

P-PSDB; AAY84066.

XX

Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit.

PT

Disclosure; Fig 28; 151pp; English.

XX

The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker

CC

improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter

CC

region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region.

CC

The method is used to produce proteins in plants. The linker propeptide

CC


```

XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX DR WPI; 2000-246564/21.
XX DR P-PSDB; AAY84067.
XX PT Improving expression of polyproteins in plants involves coexpression of
XX PT two or more proteins in plants within a single transcription unit.
XX PS Disclosure; Fig 29; 151pp; English.
XX CC The present sequence encodes a protein of the invention, comprising the
XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX CC (AMP) 1, antifungal protein 2 (RsAFP2), HsAFP1 and AceAMP1, linked by
XX CC linker propeptides of the invention. The specification describes methods
XX CC for improving expression levels of one or more proteins in a transgenic
XX CC plant. The method comprises inserting a DNA sequence having a promoter
XX CC region operably linked to two or more protein encoding regions separated
XX CC by a DNA sequence coding for a linker propeptide and a terminator region.
XX CC The method is used to produce proteins in plants. The linker propeptide
XX CC comprising a cleavage site, whereby the expressed polypeptide is post-
XX CC translationally processed into the component protein molecules. The
XX CC propeptide sequence is rich in amino acids A, V, S and T and contains
XX CC dipeptidic sequences consisting of either two acidic, two basic or one
XX CC acidic and one basic residue as a cleavable linker sequence
XX SQ Sequence 1093 BP; 278 A; 271 C; 287 G; 257 T; 0 U; 0 Other;
Query Match 38.1%; Score 170; DB 3; Length 1093;
Best Local Similarity 84.3%; Pred. No. 1.5e-36;
Matches 204; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 65 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 124
QY 215 CTGTGCGCAATACGGGACATTTGTGCAACCAATGTAATCATGCGGAGGTCGGCCCATGG 274
DB 125 CTGTGCGCAACACGGGACATTTGTGCAACCAATGTAATCATGCGGAGGTCGGCCCATGG 184
QY 275 AGCGTGTCTATGTCGCTTAACCGGAAACACATGTTTCTGTACTTCAATTGTAAAAAGC 334
DB 185 AGCGTGTCTATGTCGCTTAACCGGAAACACATGTTTCTGTACTTCAATTGTAAAAAGC 244
QY 335 CGAAAGAGCTTGTCTAAGACAAACTTAAAG---CCGAAACAACTGCTCAAGACAAACTTAA 391
DB 245 TGAGGAAGCTGCTGCTGCTATTCTCTGAAGCTTCTGAAGAACTTGTCTCAAGGAAGCTCC 304
QY 392 TG 393
DB 305 TG 306
RESULT 14
ID AAZ99324 standard; DNA; 522 BP.
XX AC AAZ99324;
XX DT 03-JUL-2000 (first entry)
XX DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.
XX KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
XX KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
XX OS Synthetic.
XX OS Dahlia merckii.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT misc_feature 160..309
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FT misc_feature /note= "encodes DmAMP1"
FT 358..510
/*tag= b
FT /note= "encodes RsAFP2"
XX PN WO200011175-A1.
XX PD 02-MAR-2000.
XX PF 17-AUG-1999; 99WO-GB002716.
XX PR 18-AUG-1998; 98GB-00018001.
XX PR 04-DEC-1998; 98GB-00026753.
XX PA (ZENEC) ZENECA LTD.
XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX DR WPI; 2000-246564/21.
XX DR P-PSDB; AAY84057.
XX PT Improving expression of polyproteins in plants involves coexpression of
XX PT two or more proteins in plants within a single transcription unit.
XX PS Example 2; Fig 8; 151pp; English.
XX CC The present sequence encodes a protein of the invention, comprising the
XX CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
XX CC propeptide of the invention. The specification describes methods for
XX CC improving expression levels of one or more proteins in a transgenic
XX CC plant. The method comprises inserting a DNA sequence having a promoter
XX CC region operably linked to two or more protein encoding regions separated
XX CC by a DNA sequence coding for a linker propeptide and a terminator region.
XX CC The method is used to produce proteins in plants. The linker propeptide
XX CC comprising a cleavage site, whereby the expressed polypeptide is post-
XX CC translationally processed into the component protein molecules. The
XX CC propeptide sequence is rich in amino acids A, V, S and T and contains
XX CC dipeptidic sequences consisting of either two acidic, two basic or one
XX CC acidic and one basic residue as a cleavable linker sequence
XX SQ Sequence 522 BP; 147 A; 119 C; 127 G; 129 T; 0 U; 0 Other;
Query Match 37.9%; Score 169.2; DB 3; Length 522;
Best Local Similarity 95.6%; Pred. No. 1.9e-36;
Matches 174; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 138 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 197
QY 215 CTGTGCGCAATACGGGACATTTGTGCAACCAATGTAATCATGCGGAGGTCGGCCCATGG 274
DB 198 CTGTGCGCAACACGGGACATTTGTGCAACCAATGTAATCATGCGGAGGTCGGCCCATGG 257
QY 275 AGCGTGTCTATGTCGCTTAACCGGAAACACATGTTTCTGTACTTCAATTGTAAAAAGC 334
DB 258 AGCGTGTCTATGTCGCTTAACCGGAAACACATGTTTCTGTACTTCAATTGTAAAAAGC 317
QY 335 CG 336
DB 318 TG 319
RESULT 15
ID AAZ54387 standard; DNA; 460 BP.
XX AC AAZ54387;
XX DT 11-APR-2001 (first entry)
XX DE Plant defensin coding sequence.

```

XX Defensin; disease; fungus; resistance; transgenic plant; vaccine;
KW immunisation; antibody; crop protection; ds.
XX Dimorphotheca sinuata.
OS
XX
XX Key Location/Qualifiers
FH CDS 25..351
FT /*tag= a
FT /product= "Plant defensin"
XX
FN WO200068405-A2.
XX
XX PD 16-NOV-2000.
XX
XX PF 03-MAY-2000; 2000WO-US011952.
XX
XX PR 07-MAY-1999; 99US-0133039P.
XX
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX PI Miao G, Weng Z, Famodu OO;
XX
XX WPI; 2001-024871/03.
DR P-PSDB; AAB04046.
XX
PT Isolated polynucleotides encoding plant defensins, useful for creating
PT transgenic plants with higher or lower levels of defensin polypeptides,
PT especially for increasing disease (e.g. fungal) resistance and stress
PT tolerance.
XX
XX Claim 2; Page 37; 50pp; English.
XX
CC Nucleotides encoding plant defensins can be used to create transgenic
CC plants in which plant defensin polypeptides are present at higher or
CC lower levels than normal, or in cell types or developmental stages in
CC which they are not normally found. This has the effect of altering the
CC level of disease (e.g. fungal) resistance and stress tolerance in those
CC cells. The defensin polypeptides are useful for immunising animals to
CC produce polyclonal or monoclonal antibodies. These antibodies are useful
CC for screening cDNA expression libraries to isolate full-length plant
CC defensin cDNA clones
XX
SQ Sequence 460 BP; 160 A; 83 C; 102 G; 115 T; 0 U; 0 Other;

Query Match 37.8%; Score 168.6; DB 5; Length 460;
Best Local Similarity 81.6%; Pred. No. 2.6e-36;
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGGTCGGGAAA 214
Db 87 AGAAATCGCGACTGTGAGAGTGCACTATGTGAGAAAGCTAGCAAGACATGGTCAGGCAA 146

QY 215 CTGTGGCAATACGGGACATTTGTGACAAACAATGTAAATCATGGAGGGTGGGCCCATGG 274
Db 147 CTGTGGCAACACGGGACACTGTGACGACAGTGAAGTCGTGGGAGACTGCAGGCCCATGG 206

QY 275 AGCGTGTCATGTGCTTAACGGGAACACATCTGTTCTTCTTACTCAATTGTTAAAGAC 334
Db 207 TCGGTGTATGTGCGGTGGGAAACACATGTGCTTCTTCTTACTCAATTGTTAAAGAC 266

QY 335 CGAAAGAGTGTCTCAAGCAAACTTTAAAGCCGAACTCGCTCAAGCAAACTTAATG 393
Db 267 CGAAAGAGTGTGCGCAAGCAAGCTCAACGCTGMAAAATTCGCCCGTGATGACGTTAAG 325

Search completed: March 18, 2005, 13:52:15
Job time : 388 secs

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OM nucleic - nucleic search, using sw model

Run on: March 18, 2005, 12:55:37 ; Search time 136 Seconds
(without alignments)
5366.025 Million cell updates/sec

Title: US-09-763-019-5
Perfect score: 446
Sequence: 1 atggtgaatcgggtggtgc.....ttccaaacgttgaaacatccg 446

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
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5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154.2	34.6	565	4	US-09-589-733C-6
2	99.4	22.3	150	1	US-08-377-687-31
3	99.4	22.3	150	1	US-08-777-192-31
4	99.4	22.3	150	3	US-08-971-982-31
5	91.4	20.5	150	1	US-08-377-687-33
6	91.4	20.5	150	1	US-08-777-192-33
7	91.4	20.5	150	3	US-08-971-982-33
8	86.6	19.4	150	1	US-08-377-687-34
9	86.6	19.4	150	1	US-08-777-192-34
10	86.6	19.4	150	3	US-08-971-982-34
11	58.4	13.1	147	1	US-08-377-687-36
12	58.4	13.1	147	1	US-08-777-192-36
13	58.4	13.1	147	3	US-08-971-982-36
14	44.6	10.0	270	1	US-08-627-706-14
15	44.6	10.0	270	3	US-09-103-489-14
16	44.6	10.0	270	4	US-09-829-381D-14
17	44.6	10.0	286	1	US-08-627-706-12
18	44.6	10.0	286	3	US-09-103-489-12
19	44.6	10.0	286	4	US-09-829-381D-12
20	40.8	9.1	500	1	US-08-627-706-9
21	40.8	9.1	500	3	US-09-103-489-9
22	40.8	9.1	500	4	US-09-829-381D-9
23	40.8	9.0	414	1	US-08-377-687-48
24	40.8	9.0	414	1	US-08-777-192-48
25	40.8	9.0	414	3	US-08-971-982-48
26	40.8	9.0	414	3	US-09-077-951-19
27	40.8	9.0	414	4	US-09-077-948A-45

28	39	8.7	288	1	US-08-377-687-58	Sequence 58, Appl
29	39	8.7	288	1	US-08-777-192-58	Sequence 58, Appl
30	39	8.7	288	3	US-08-971-982-58	Sequence 58, Appl
C 31	38.6	8.7	112	4	US-09-589-733C-32	Sequence 32, Appl
C 32	38.6	8.7	7218	1	US-08-232-463-14	Sequence 14, Appl
33	38.4	8.6	1346	4	US-09-589-733C-9	Sequence 9, Appl
34	38.2	8.6	60	1	US-08-377-687-32	Sequence 32, Appl
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37	37.4	8.4	1141	4	US-09-806-708B-22	Sequence 22, Appl
C 38	35.2	7.9	601	4	US-09-949-016-154963	Sequence 154963,
C 39	35.2	7.9	601	4	US-09-949-016-178474	Sequence 178474,
C 40	35.2	7.9	942	4	US-09-270-767-3330	Sequence 3330, Ap
C 41	35.2	7.9	942	4	US-09-270-767-18612	Sequence 18612, A
C 42	35.2	7.9	99830	4	US-09-949-016-16859	Sequence 16859, A
C 43	35.2	7.9	385136	4	US-09-949-016-16073	Sequence 16073, A
44	35	7.8	51835	4	US-09-949-016-17101	Sequence 17101, A
45	35	7.8	52032	4	US-09-949-016-11789	Sequence 11789, A

ALIGNMENTS

RESULT 1
US-09-589-733C-6
; Sequence 6, Application US/09589733C
; Patent No. 6677503
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Craata, Oswald R.
; APPLICANT: Duwick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; TITLE OF INVENTION: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/09589,733C
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-09-589-733C-6

Query Match	34.6%	Score 154.2;	DB 4;	Length 565;
Best Local Similarity	76.5%	Pred. No. 8.6e-38;		
Matches 189;	Conservative	0;	Mismatches 58;	Indels 0;
Gaps	0;			
QY	155	AGATATCCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA	214	
Db	99	AGAAATCGATCGGTGAAAGGAGATTTATGTGAGAGGCGAAGCCAGACATGTCGGGAA	158	
QY	215	CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCGCCCATGG	274	
Db	159	ATGTGGCAAGACAAACACTGTGTGACCACTGTGTGAGGAGGTTGGAGGAGGTCAGCCATGG	218	
QY	275	AGCGTGTGTCATGTCGTAACCGGAAAACACATGTGTTTCTGTACTTTCAATTTGTAAGAAAGC	334	
Db	219	AGCTTGTGTCATGTCGTAACCGGAAAACACATGTGTTTCTGTACTTTCAATTTGTAAGAAAGC	278	
QY	335	CGAAAGCTTGTCTAAGACAAACTTAAAGCCGGAACACTCGCTCAAGACAACTTAATGC	394	
Db	279	CCAGAAGTTGGTCTAGGATAAATCTCAGAGCGGAGAGCTCGCCAGGAGAGATTGAACC	338	
QY	395	CCAAAAG 401		
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```
RESULT 2
US-08-377-687-31
; Sequence 31, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 31:
; LENGTH: 150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-377-687-31

; Query Match 22.3%; Score 99.4; DB 1; Length 150;
; Best Local Similarity 79.2%; Pred. No. 4.6e-21;
; Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 177 GAACATATCGGAGAAAGCTAGCAACACATGTCGGGAAACTGTGGCAATACGGGCAATTGT 236
Db 1 GAGCTTTGCGAGAGGCTTCTTAAGACTTGGTCTGGAAACTCGGAAACACTGGGCAATTGC 60

Qy 237 GACACCAATGTAATCATGCGGAGGTGCGGCCCATGGAGCGTGTCTATGTCGTAACGGG 296
Db 61 GATRAACCAATGCAAGTCTTTGGAGGAGCTGCTCATGAGCTTGCCATGTTAGAACCGGA 120

Qy 297 AAACACATGTGTTTCTGTTACTTCAATTG 325
Db 121 AAGCATATGTGCTTCTGCTACTTCAACTG 149

RESULT 3
US-08-777-192-31
; Sequence 31, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
```

```
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 31:
; LENGTH: 150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-777-192-31

; Query Match 22.3%; Score 99.4; DB 1; Length 150;
; Best Local Similarity 79.2%; Pred. No. 4.6e-21;
; Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 177 GAACATATCGGAGAAAGCTAGCAACACATGTCGGGAAACTGTGGCAATACGGGCAATTGT 236
Db 1 GAGCTTTGCGAGAGGCTTCTTAAGACTTGGTCTGGAAACTCGGAAACACTGGGCAATTGC 60

Qy 237 GACACCAATGTAATCATGCGGAGGTGCGGCCCATGGAGCGTGTCTATGTCGTAACGGG 296
Db 61 GATRAACCAATGCAAGTCTTTGGAGGAGCTGCTCATGAGCTTGCCATGTTAGAACCGGA 120

Qy 297 AAACACATGTGTTTCTGTTACTTCAATTG 325
Db 121 AAGCATATGTGCTTCTGCTACTTCAACTG 149

RESULT 4
US-08-971-982-31
; Sequence 31, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
```

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SSE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-377-687-33

Query Match 20.5%; Score 91.4; DB 1; Length 150;
Best Local Similarity 75.8%; Pred. No. 1.4e-18;
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0

QY 177 GAACATATGCGAGAAAGCTAGCAAGACATGCTGCGGAAACTGTGGCAATACGGGACATTGT 236
Db 1 GAGCTTTGCGAGAAGGCTTCTAGAGCTTGGTCTCGAAACTCGGAAACACATAAGCATTGC 60

QY 237 GACAACCAATGTAATCATCGGAGGGTGGCGCCCATGGAGCGTGTGCCTAACGGG 296
Db 61 GATGATCAATGCAAGTCTTGGGAGGAGCTGCTCATGGAGCTTGCATGTTAGAAAACGGA 120

QY 297 AAACACATGTTTCTGTTACTTCAATTG 325
Db 121 AAGCATATGCTTCTGCTACTTCAACTG 149

RESULT 6
US-08-777-192-33
; Sequence 33, Application US/08777192
; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,192
; FILING DATE:
; CLASSIFICATION:

```

;;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-777-192-33

Query Match 20.5%; Score 91.4; DB 1; Length 150;
Best Local Similarity 75.8%; Pred. No. 1.4e-18;
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 177 GAACTATGCGAGAAAGCTAGCAAGACATGGTCGGGAAACTGTGGCAATACGGGACATTGT 236
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Db 1 GAGCTTTGCGAGAAGGCTTCTAAGACTTGGTCTGGAAACTGCGGAAACACTAAGCATTCG 60

QY 237 GACAACCAATGTAATCATGGGAGGGTGGCGCCCATGGAGCGTGTCTATGTCGTAACGGG 296
|||
Db 61 GATGATCAATGCAAGTCTTGGGAGGAGCTGCTCATGGAGCTTGCCATGTTAGAAACGGA 120

QY 297 AAACACATGTGTTCTGTTACTTCAATTG 325
|||
Db 121 AAGCATATGTGTTCTGCTACTTCAACTG 149

RESULT 7
US-08-971-982-33
; Sequence 33, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; CAMMUE, BRUNO P.A.
; OSBORN, RUPERT W.
; REES, SARAH B.
; TERRAS, FRANKY R.G.
; VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARB & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-NO. 6187904-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:

;;
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-08-971-982-33

Query Match 20.5%; Score 91.4; DB 3; Length 150;
Best Local Similarity 75.8%; Pred. No. 1.4e-18;
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 177 GAACTATGCGAGAAAGCTAGCAAGACATGGTCGGGAAACTGTGGCAATACGGGACATTGT 236
|||
Db 1 GAGCTTTGCGAGAAGGCTTCTAAGACTTGGTCTGGAAACTGCGGAAACACTAAGCATTCG 60

QY 237 GACAACCAATGTAATCATGGGAGGGTGGCGCCCATGGAGCGTGTCTATGTCGTAACGGG 296
|||
Db 61 GATGATCAATGCAAGTCTTGGGAGGAGCTGCTCATGGAGCTTGCCATGTTAGAAACGGA 120

QY 297 AAACACATGTGTTCTGTTACTTCAATTG 325
|||
Db 121 AAGCATATGTGTTCTGCTACTTCAACTG 149

RESULT 8
US-08-377-687-34
; Sequence 34, Application US/08377687
; Patent No. 5538525
; GENERAL INFORMATION:
; APPLICANT: BROEKERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARB & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/377,687
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both

TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-377-687-34

Query Match 19.4%; Score 86.6; DB 1; Length 150;
Best Local Similarity 73.8%; Pred. No. 4.3e-17;
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATATGCGAGAAAGCTAGCAAGACATGCTGGGAAACTGTGGCAATACGGGACATTGT 236
DB 1 GAGCTTTGCGAAGGCTTCTAAGACTTGGTCTGGAACCTGCGAAACACTAAGCAATTGC 60

QY 237 GACAAACCAATGTAATCATGAGGAGGTGGGCCCATGGAGCGTGTCTCATGTGGTAAACGGG 296
DB 61 GATAACAAGTGAAGCTTCTAAGACTTGGTCTGGAACCTGCGAAACACTAAGCAATTGC 60

QY 297 AAACACATGTTCTTCTGTTACTTCAATTG 325
DB 121 AAGCATATGTGCTTCTGCTACTTCAACTG 149

RESULT 9
US-08-777-192-34
Sequence 34, Application US/08777192
Patent No. 5824869
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEIDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/777,192
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-08-777-192-34

Query Match 19.4%; Score 86.6; DB 1; Length 150;
Best Local Similarity 73.8%; Pred. No. 4.3e-17;
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATATGCGAGAAAGCTAGCAAGACATGCTGGGAAACTGTGGCAATACGGGACATTGT 236
DB 1 GAGCTTTGCGAAGGCTTCTAAGACTTGGTCTGGAACCTGCGAAACACTAAGCAATTGC 60

QY 237 GACAAACCAATGTAATCATGAGGAGGTGGGCCCATGGAGCGTGTCTCATGTGGTAAACGGG 296
DB 61 GATAACAAGTGAAGCTTCTAAGACTTGGTCTGGAACCTGCGAAACACTAAGCAATTGC 60

QY 297 AAACACATGTTCTTCTGTTACTTCAATTG 325
DB 121 AAGCATATGTGCTTCTGCTACTTCAACTG 149

RESULT 9
US-08-777-192-34
Sequence 34, Application US/08777192
Patent No. 5824869
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEIDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/777,192
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-08-777-192-34

Query Match 19.4%; Score 86.6; DB 1; Length 150;
Best Local Similarity 73.8%; Pred. No. 4.3e-17;
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATATGCGAGAAAGCTAGCAAGACATGCTGGGAAACTGTGGCAATACGGGACATTGT 236
DB 1 GAGCTTTGCGAAGGCTTCTAAGACTTGGTCTGGAACCTGCGAAACACTAAGCAATTGC 60

QY 237 GACAAACCAATGTAATCATGAGGAGGTGGGCCCATGGAGCGTGTCTCATGTGGTAAACGGG 296
DB 61 GATAACAAGTGAAGCTTCTAAGACTTGGTCTGGAACCTGCGAAACACTAAGCAATTGC 60

QY 297 AAACACATGTTCTTCTGTTACTTCAATTG 325
DB 121 AAGCATATGTGCTTCTGCTACTTCAACTG 149

RESULT 10
US-08-971-982-34
Sequence 34, Application US/08971982
Patent No. 6187904
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEIDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/971,982
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-08-971-982-34

Query Match 19.4%; Score 86.6; DB 3; Length 150;
Best Local Similarity 73.8%; Pred. No. 4.3e-17;
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATATGCGAGAAAGCTAGCAAGACATGCTGGGAAACTGTGGCAATACGGGACATTGT 236
DB 1 GAGCTTTGCGAAGGCTTCTAAGACTTGGTCTGGAACCTGCGAAACACTAAGCAATTGC 60

QY 237 GACAAACCAATGTAATCATGAGGAGGTGGGCCCATGGAGCGTGTCTCATGTGGTAAACGGG 296
DB 61 GATAACAAGTGAAGCTTCTAAGACTTGGTCTGGAACCTGCGAAACACTAAGCAATTGC 60

RESULT 12
US-08-777-192-36

RESULT 13
US-08-971-982-36
; Sequence 36, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROKAERT, WILLEM H
; CAMMUE, BRUNO P.A.
; OSBORN, RUPERT W.
; REES, SARAH B.
; TERRAS, FRANKY R.G

VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-NO. 6187504-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-08-971-982-36
Query Match 13.1%; Score 58.4; DB 3; Length 147;
Best Local Similarity 66.9%; Pred. No. 2.5e-08;
Matches 99; Conservative 0; Mismatches 46; Indels 3; Gaps 1;
Qy 178 AACTATGCGAGAACTAGCAGACATGTCGGGAACTGTGGCAATACGGACATTGTG 237
Db 2 ACCTTGCGAGAGCTTCTTACTTGGACTGGAACTGCGGAACTGCGAACTGCGACATTGCG 61
Qy 238 ACAACCAATGTAATCATGGGGGGTGGCCCATGGAGCGTGTCTATGCGTAACGGGA 297
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Qy 298 AACACATGTGTTCTGTACTTCAATTG 325
Db 119 ACTGGAAGTGCTCTGCTACTTCGATTG 146
RESULT 14
US-08-627-706-14
; Sequence 14, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; CONTROLLING PLANT PATHOGENIC FUNGI
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri

COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-627-706-14
Query Match 10.0%; Score 44.6; DB 1; Length 270;
Best Local Similarity 53.8%; Pred. No. 0.00065;
Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
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Db 95 CAATGTTGGATGCCAAGGTTGTGCGAGACCAAGTGGGACATGTCAGGAGTTTGTGGGA 154
Qy 223 ATACGGGACATTGTGACAAACCAATGTAATCATGGGAGGGTGGCCCATGGAGCGTGC 282
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Qy 283 ATGTGCGTAAACGGGAAACACATGTTCTGTCTTCAATTTGTAATAAG 333
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RESULT 15
US-09-103-489-14
; Sequence 14, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; CONTROLLING PLANT PATHOGENIC FUNGI
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 6215048th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:

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; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-103-489-14

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Query Match      10.0%; Score 44.6; DB 3; Length 270;
Best Local Similarity 53.8%; Pred. No. 0.00065;
Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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QY 223 ATACGGGACATTGTGACACCAATGTAATCATGGAGGGTCCGGCCCATGGAGCGTGTG 282
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 155 ACAACAATGTCATGTCAGGAAACCAATGCAGAAACCTTTGAAAGAGCAGACACGGATCTTGA 214
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 283 ATGTGCGTAACGGGAAACACATGTGTTCTGTCTTCTTCAATTGTAATAAAG 333
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 215 ACTATGTCTTCCAGCTCACAATGTATTTGTTACTTCTCCATGTTAATAAG 265
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Job time : 137 secs

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OM nucleic - nucleic search, using sw model

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Title: US-09-763-019-5
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Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:*

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- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
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- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	168.6	37.8	503	15	US-10-178-449A-1
5	161	36.1	461	15	US-10-178-449A-46
6	156.4	35.1	457	15	US-10-178-449A-13
7	156.4	35.1	463	15	US-10-178-449A-9
8	156.4	35.1	603	15	US-10-178-449A-11
9	154.8	34.7	458	15	US-10-178-449A-21
10	154.8	34.7	460	15	US-10-178-449A-17
11	154.2	34.6	565	17	US-10-636-396-6

12	154.2	34.6	565	18	US-10-636-026-6
13	153.2	34.3	464	15	US-10-178-449A-19
14	153.2	34.3	472	15	US-10-178-449A-23
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18	88.2	19.8	610	15	US-10-178-449A-29
19	88.2	19.8	658	15	US-10-178-449A-7
20	87.8	19.7	156	15	US-10-178-449A-34
21	86.6	19.4	150	9	US-09-759-584-34
22	85.8	19.2	501	15	US-10-178-449A-5
23	74.8	16.8	250	15	US-10-178-449A-36
24	65.8	14.8	373	9	US-09-770-696-283
25	58.4	13.1	147	9	US-09-759-584-35
26	56.6	12.7	470	14	US-10-178-213-88
27	47.8	10.7	499	15	US-10-178-449A-25
28	47.8	10.7	517	15	US-10-178-449A-27
29	44.6	10.0	270	9	US-09-829-381A-14
30	44.6	10.0	270	17	US-10-681-972-14
31	44.6	10.0	286	9	US-09-829-381A-12
32	44.6	10.0	286	17	US-10-681-972-12
33	41.6	9.3	1616	9	US-09-732-561-21
34	41.2	9.2	400	9	US-09-732-561-15
35	40.8	9.1	500	9	US-09-829-381A-9
36	40.8	9.1	500	17	US-10-681-972-9
37	40.2	9.0	243	9	US-09-938-842A-2046
38	40.2	9.0	243	11	US-09-938-842A-2046
39	40	9.0	414	9	US-09-759-584-48
40	40	9.0	414	13	US-10-006-252A-19
41	40	9.0	414	17	US-10-388-361A-45
42	39.6	8.9	335913	10	US-09-754-853A-2
43	39.6	8.9	335913	10	US-09-754-853A-3
44	39.2	8.8	3673778	16	US-10-312-841-1
45	39	8.7	288	9	US-09-759-584-58

ALIGNMENTS

RESULT 1

US-10-178-449A-48
; Sequence 48, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnall, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Vernonia mespilifolia
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 480_515, 521, 529
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (25)....(372)
US-10-178-449A-48

Query Match      47.0%; Score 209.4; DB 15; Length 529;
Best Local Similarity 82.5%; Pred. No. 4.2e-48;
Matches 240; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
Db 78 AGAATCTCGAGTGTGAGAGCAGAGCTATGCGAGAAAGCTAGCAAGACATGTCAGGCAA 137

QY 215 CTGTGCAATACGGGACATTTGTGACAACTTAAAGCCGAACTCGCTCAAGACAACTTAATGC 274
Db 138 CTGTGGCAACACAGGACATTTGTGATAATCAGTGTAACTGATGAGGAGGCTGAGCCCATGG 197

QY 275 AGCGTGTATGTCGTTAAGCGGAAACACATGTGTTCTTCTTACTTCAATTTGTAAGAAAGC 334
Db 198 AGCTTGTATGTCGCTGAGGAGGAAACACATGTGCTTTTGTATTCAATTTGTAAGAAAGC 257

QY 335 CGAAAGCTTGTCTCAAGACAACTTAAAGCCGAACTCGCTCAAGACAACTTAATGC 394
Db 258 TGAAGAACTCGCTCAAGATAGTAAAGCTGAGAGGCTTGAAGAGACAACTCAAGGC 317

QY 395 CAAAAGCTTGACCGTGTATGCAAGAAAGTGGTTCCTCAAAACGTTGAACATCC 445
Db 318 AGATAAGTTTGACCATGATGCAAAAGAAAGTAGTAGTACCAATGTCGAACATCC 368

RESULT 2
US-10-178-449A-31
; Sequence 31, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Vernonia mespilifolia
US-10-178-449A-31

Query Match      45.5%; Score 203; DB 15; Length 579;
Best Local Similarity 81.1%; Pred. No. 2.7e-46;
Matches 236; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
Db 92 AGAATCTCGAGTGTGAGAGCAGAGCTATGCGAGAGAGCTAGCAAGACATGTCAGGCAA 151

QY 215 CTGTGCAATACGGGACATTTGTGACAACTTAAAGCCGAACTCGCTCAAGACAACTTAATGC 274
Db 152 CTGTGGCAACACAGGACATTTGTGATAATCAGTGTAACTGATGAGGAGGCTGAGCCCATGG 211

QY 275 AGCGTGTATGTCGCTGAGGAGGAAACACATGTGTTCTTCTTACTTCAATTTGTAAGAAAGC 334
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Db 212 AGCTTGTATGTCGCTGAGGAAACACATGCTGCTTTTGTCTATTTCATTTGTAAGAAAGC 271
QY 335 CGAAAGCTTGTCTCAAGACAACTTAAAGCCGAACTCGCTCAAGACAACTTAATGC 394
Db 272 TGAAGAACTCGCTCAAGATAGTAAAGCTGAGAGGCTTGAAGAGACAACTCAAGGC 331
QY 395 CAAAAGCTTGACCGTGTATGCAAGAAAGTGGTTCCTCAAAACGTTGAACATCC 445
Db 332 AGATAAGTTTGACCATGATGCAAAAGAAAGTAGTAGTACCAATGTCGAACATCC 382

RESULT 3
US-10-178-449A-3
; Sequence 3, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Dimorphotheca sinuata
US-10-178-449A-3

Query Match      37.8%; Score 168.6; DB 15; Length 460;
Best Local Similarity 81.6%; Pred. No. 1e-36;
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
Db 87 AGAATCGGACTGTGAGAAAGTGCACCTATGTGAGAAAGCTAGCAAGACATGTCAGGCAA 146

QY 215 CTGTGCAATACGGGACATTTGTGACAACTTAAATCATGAGGAGGTCGGCCCATGG 274
Db 147 CTGTGGCAACACAGGACATGTCGACGCCAGCTAGTAAAGTCTGTTGGAGACTCGAGCCCATGG 206

QY 275 AGCGTGTATGTCGCTAAACGGGAAACACATGCTGCTTTCTGTTACTTCAATTTGTAAGAAAGC 334
Db 207 TGCCTGTATGTCGCTGTTGGGAAACACATGCTGCTTCTGCTCTTCAATTTGTAAGAAAGC 266

QY 335 CGAAAGCTTGTCTCAAGACAACTTAAAGCCGAACTCGCTCAAGACAACTTAATGC 393
Db 267 CGAAAGCTTGCCCAAGACAACTCAACGCTGAAAAATTCGGCCGCTGATGACGCTTAAG 325

RESULT 4
US-10-178-449A-1
; Sequence 1, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
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; APPLICANT: Miao, Guo-Hua
; APPLICANT: Prenail, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Dimorphotheca sinuata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 321, 349, 416, 458, 474, 479, 482, 502
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-1

Query Match      37.8%; Score 168.6; DB 15; Length 503;
Best Local Similarity 81.6%; Pred. No. 1.1e-36;
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 80 AGAATCGCATCGTGTGAGAAAGTGCATGTGAGAAAGCTAGCAAGACATGTCAGGCAA 139

QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGAGGGTGGCGCCCATGG 274
DB 140 CTGTGGCAACAGGACACTGTGACGACCACTGTGAGTAAAGTGTGAGAGAGTGCAGCCCATGG 199

QY 275 AGCGTGTGCATGTGCGTAACGGGAAACACATGTGTTCTGTACTTCAATTTGTAAGAAAGC 334
DB 200 TCGGTGTGCATGTGCGTGGTGGGAAACACATGTGTTCTGTACTTCAATTTGTAAGAAAGC 259

QY 335 CGAAAAGCTTGTCTAAGCAAACTTTAAAGCCGAAACACTCGCTCAAGCAAACTTTAATG 393
DB 260 CGAAAAGCTTGTCTAAGCAAACTTTAAAGCCGAAACACTCGCTCAAGCAAACTTTAATG 318

RESULT 5
US-10-178-449A-46
; Sequence 46, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Prenail, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 424, 436
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-13

Query Match      35.1%; Score 156.4; DB 15; Length 457;
Best Local Similarity 77.2%; Pred. No. 2.6e-33;
Matches 190; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
```

```
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Helianthus annuus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)...(340)
US-10-178-449A-46

Query Match      36.1%; Score 161; DB 15; Length 461;
Best Local Similarity 77.9%; Pred. No. 1.4e-34;
Matches 194; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
DB 76 AGAATCGCATCGTGTGAGAAAGTATGAGAAAGGCAAGCAAGACATGTCGGGAAA 135

QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGAGGGTGGCGCCCATGG 274
DB 136 ATGTGGCAACACAGACACTGTGACGACCACTGTGCAAGTCTTGGGAGGGTGCAGCCCATGG 195

QY 275 AGCGTGTGCATGTGCGTAACGGGAAACACATGTGTTCTGTACTTCAATTTGTAAGAAAGC 334
DB 196 AGCTTGTGCATGTGCGGCGTGGGAAACACATGTGTTCTGTACTTCAACTGTTCGAAAGC 255

QY 335 CGAAAAGCTTGTCTAAGCAAACTTTAAAGCCGAAACACTCGCTCAAGCAAACTTTAATG 394
DB 256 CGAAAAGCTTGTCTAAGCAAACTTTAAAGCCGAAACACTCGCTCAAGCAAACTTTAATG 315

QY 395 CGAAAAGCT 403
DB 316 CGAAAAGCT 324

RESULT 6
US-10-178-449A-13
; Sequence 13, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Prenail, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 424, 436
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-13

Query Match      35.1%; Score 156.4; DB 15; Length 457;
Best Local Similarity 77.2%; Pred. No. 2.6e-33;
Matches 190; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
```

Db 91 AGAAATCGGATCGGTGAAGGAGAACTATGTGAGAGGCAAGCAAGACATGGTCTGGAAA 150
QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGGAGGGTGGCGCCCATGG 274
Db 151 TTGTGGTACACAGACATTTGTGACCAACCAATGCAAGTCTTTGGGAGGGTGCAGCCCATGG 210
QY 275 AGCGTGTCTATGTCGCTGTAACGGGAAACACATGTTCTTCTTACTTCAATTTGTAAGAAAGC 334
Db 211 AGCTTGTCTATGTCGCGGTGGGAAACACATGTTCTTCTTACTTCAATTTGTAAGAAAGC 270
QY 335 CGAAAGCTTGTCTAAGACAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAATGC 394
Db 271 CGAGAGATGGCCAGGATAAACTCGAGCTGAAGAGCTTGCCAGGAGAGATTTGAAGC 330
QY 395 CCAAAA 400
Db 331 TGAANA 336

RESULT 7

US-10-178-449A-9
; Sequence 9, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Prenail, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 413
; OTHER INFORMATION: n = A,T,C or G

US-10-178-449A-9

Query Match 35.1%; Score 156.4; DB 15; Length 463;
Best Local Similarity 77.2%; Pred. No. 2.7e-33;
Matches 190; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAACTAGCAAGAGCTAGCAAGACATGGTCGGGAAA 214
Db 94 AGAAATCGGATCGGTGAAGGGAGAACTATGTGAGAGGCAAGCAAGACATGGTCTGGAAA 153
QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGGAGGGTGGCGCCCATGG 274
Db 154 TTGTGGTAAACAAGACATTTGTGACGACCAATGTCAGTCTTTGGGAGGGTGCAGCCCATGG 213
QY 275 AGCGTGTCTATGTCGCTTAACGGGAAACACATGTTCTTCTTACTTCAATTTGTAAGAAAGC 334
Db 214 AGCTTGTCTATGTCGCGGTGGGAAACACATGTTCTTCTTACTTCCAGTGGCCCAAGC 273
QY 335 CGAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAATGC 394

Db 274 CGAGAGATGGCCAGGATTAACCTCCGAGCTGAAGAGCTTCCCAAGGAGAGATTGAAGC 333
QY 395 CCAAAA 400
Db 334 TGAANA 339

RESULT 8

US-10-178-449A-11
; Sequence 11, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Prenail, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; US-10-178-449A-11

Query Match 35.1%; Score 156.4; DB 15; Length 603;
Best Local Similarity 77.2%; Pred. No. 3e-33;
Matches 190; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAACTAGCAAGACATGGTCGGGAAA 214
Db 101 AGAAATCGGATCGGTGAAGGGAGAACTATGTGAGAGGCAAGCAAGACATGGTCTGGAAA 160
QY 215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGGGAGGGTGGCGCCCATGG 274
Db 161 TTGTGGTAAACAAGACATTTGTGACGACCAATGTCAGGAGGGTGCAGCCCATGG 220
QY 275 AGCGTGTCTATGTCGCTTAACGGGAAACACATGTTCTTCTTACTTCAATTTGTAAGAAAGC 334
Db 221 AGCTTGTCTATGTCGCGGTGGGAAACACATGTTCTTCTTACTTCCAGTGGCCCAAGC 280
QY 335 CGAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACAACTCGCTCAAGACAACTTAATGC 394
Db 281 CGAGAGATGGCCAGGATAAACTCCGAGCTGAAGAGCTTCCCAAGGAGAGATTGAAGC 340
QY 395 CCAAAA 400
Db 341 TGAANA 346

RESULT 9

US-10-178-449A-21
; Sequence 21, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua

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; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 322, 375, 402, 452
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-21

Query Match          34.7%; Score 154.8; DB 15; Length 458;
Best Local Similarity 76.8%; Pred. No. 7.4e-33;
Matches 189; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCCAGAAAGCTAGCAAGACATGGTCGGGAAA 214
    |||||
Db 72 AGAATCGGATCGGTGAGGAGAACTATGTGAGAGGCGCAAGACATGGTCGGAAA 131

QY 215 CTGTGGCAATACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCGCCCATGG 274
    |||||
Db 132 TTGTGGTAACACAGACACTGTGACGACCAATGCAAGTCTTGGAGGGTGCAGCCCATGG 191

QY 275 ACCGTGTCTATGTCGTAAACCGGAAACACATGTGTTCTGTTACTTCAATTTAAAGC 334
    |||||
Db 192 AGCTTGTCTATGTCGTGCGGGTGGGAAACACATGTGCTTCTGCTACTTCCAGTGCCTCAAGC 251

QY 335 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAACTCAAGCTCGCTCAAGCAAACTTAAAGC 394
    |||||
Db 252 CGAGAAGATGGCCAGGATAAATCTCGAGCTGAGAGCTTGCAGGAGAGATTGAAGC 311

QY 395 CCAAAA 400
    |||||
Db 312 TGAAA 317

RESULT 10
US-10-178-449A-17
; Sequence 17, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07

; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 342
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-17

Query Match          34.7%; Score 154.8; DB 15; Length 460;
Best Local Similarity 76.8%; Pred. No. 7.4e-33;
Matches 189; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCCAGAAAGCTAGCAAGACATGGTCGGGAAA 214
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Db 89 AGAATCGGATCGGTGAGGAGAACTATGTGAGAGGCGCAAGACATGGTCGGAAA 148

QY 215 CTGTGGCAATACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCGCCCATGG 274
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Db 149 TTGTGGTAACACAGACACTGTGACGACCAATGCAAGTCTTGGAGGGTGCAGCCCATGG 208

QY 275 ACCGTGTCTATGTCGTAAACCGGAAACACATGTGTTCTGTTACTTCAATTTAAAGC 334
    |||||
Db 209 AGCTTGTCTATGTCGTGCGGGTGGGAAACACATGTGCTTCTGCTACTTCCAGTGCCTCAAGC 268

QY 335 CGAAAGCTTGTCTCAAGCAAACTTAAAGCCGAACTCAAGCTCGCTCAAGCAAACTTAAAGC 394
    |||||
Db 269 CGAGAAGATGGCCAGGATAAATCTCGAGCTGAGAGCTTGCAGGAGAGATTGAAGC 328

QY 395 CCAAAA 400
    |||||
Db 329 TGAAA 334

RESULT 11
US-10-636-396-6
; Sequence 6, Application US/10636396
; Publication No. US20040073971A1
; GENERAL INFORMATION:
; APPLICANT: Bidney, Dennis L.
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jon
; APPLICANT: Hu, Xu
; APPLICANT: Lu, Guihua
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
; TITLE OF INVENTION: Genes and their Uses
; FILE REFERENCE: 5718-90
; CURRENT APPLICATION NUMBER: US/10/636,396
; CURRENT FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US/09/589,733C
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 60/140,646
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/162,904
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Helianthus annuus
US-10-636-396-6

Query Match          34.6%; Score 154.2; DB 17; Length 565;
Best Local Similarity 76.5%; Pred. No. 1.2e-32;
Matches 189; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCCAGAAAGCTAGCAAGACATGGTCGGGAAA 214
    |||||
Db 99 AGAATCGGATCGGTGAGGAGAACTATGTGAGAGGCGCAAGACATGGTCGGAAAC 158
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QY	215	CTGTGGCAATACGGGACATTGTGACAAACCAATGTAAATCATGGAGGGTGCGGCCCATGG	274
Db	159	ATGTGGCAAGACAAACACACTGTGTGATGACCAAGTCTTTGGAGGGTGCAGCCCATGG	218
QY	275	AGCGTGTCTATGTGCGTAAACGGGAAACACATGTGTTTCTGTTTACTTCAATTGTAAAAAAGC	334
Db	219	AGCTTGTCACTGTCGGCGATGGGAAACACATGTGCTTCTGTACTCTTCAACTGTGTTCCAAAGC	278
QY	335	CGAAAGCTTGTCTCAAGACAAACTTAAAGCCGAACAACTCGCTCAAGACAAACTTAAATGC	394
Db	279	CCAGAAGTTGGCTCAGGATAAACTCAGAGCGGAAGAGCTCGCCAAGGAGAAGATTGAACC	338
QY	395	CCAAAAG 401	
Db	339	CGAAAAG 345	

RESULT 12			
US-10-636-026-6			
; Sequence 6, Application US/10636026			
; Publication No. US20040111761A1			
; GENERAL INFORMATION:			
; APPLICANT: Bidney, Dennis L.			
; APPLICANT: Crasta, Oswald R.			
; APPLICANT: Duvick, Jon			
; APPLICANT: Hu, Xu			
; APPLICANT: Lu, Guihua			
; TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and			
; FILE OF INVENTION: Genes and their Uses			
; FILE REFERENCE: 5718-90			
; CURRENT APPLICATION NUMBER: US/10/636,026			
; CURRENT FILING DATE: 2003-08-07			
; PRIOR APPLICATION NUMBER: US/09/589,733C			
; PRIOR FILING DATE: 2000-06-08			
; PRIOR APPLICATION NUMBER: 60/140,646			
; PRIOR FILING DATE: 1999-06-23			
; PRIOR APPLICATION NUMBER: 60/162,904			
; PRIOR FILING DATE: 1999-11-01			
; NUMBER OF SEQ ID NOS: 41			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 6			
; LENGTH: 565			
; TYPE: DNA			
; ORGANISM: Helianthus annuus			
US-10-636-026-6			

Query Match		34.6%;	Score 154.2;	DB 18;	Length 565;
Best Local Similarity		76.5%;	Pred. No. 1.2e-32;	Mismatches 58;	Indels 0;
Matches 189;		Conservative 0;			

QY	155	AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA	214
Db	99	AGAAATCGGATCGGTGAAGCGAATATGTGAGAAGCGCAAGCATGTCGGAAC	158
QY	215	CTGTGGCAATACGGGACATTGTGACACCAATGTAAATCATGGAGGGTGCGGCCCATGG	274
Db	159	ATGTGGCAAGACAAACACACTGTGTATGACCAAGTCTTGGAGGGTGCAGCCCATGG	218
QY	275	AGCGTGTCTATGTGCGTAAACGGGAAACACATGTGTTTCTGTTTACTTCAATTGTAAAAAAGC	334
Db	219	AGCTTGTCACTGTCGGCGATGGGAAACACATGTGCTTCTGTACTCTTCAACTGTGTTCCAAAGC	278
QY	335	CGAAAGCTTGTCTCAAGACAAACTTAAAGCCGAACAACTCGCTCAAGACAAACTTAAATGC	394
Db	279	CCAGAAGTTGGCTCAGGATAAACTCAGAGCGGAAGAGCTCGCCAAGGAGAAGATTGAACC	338
QY	395	CCAAAAG 401	
Db	339	CGAAAAG 345	

RESULT 13	
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; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 368
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-23
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Best Local Similarity 76.4%; Pred. No. 2.1e-32;
Matches 188; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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Db 86 AGAAATCGGATCGGTGAAGGAGAACTATGTGAGAGGCAAGCAAGACATGTCGTGAAA 145

Qy 215 CTGTGGCAATACGGGACATTTGTGACAACTTAAATCATGGGAGGGTGGGCCCATGG 274
Db 146 TTGTGTTAAACACAGACATTTGTGACCAATGCAAGTCTTGGGAGGGTGCAGCCCATGG 205

Qy 275 AGCGTGTGTCATGTGCTTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAAAAAGC 334
Db 206 AGCTTGTGTCATGTGCGCGGTGGGAAACACATGTGCTTCTGCTACTTCCAGTGCCTCAAGC 265

Qy 335 CGAAAAGCTTCTCAAGCAAACTTAAAGCCGAACTCGCTCAAGCAAACTTAATGTC 394
Db 266 CGAGAAGATGCCCCAGGATTAACCTCCGAGCTGAAGAGCTTGCCCAAGGAGAGATTGAAGT 325

Qy 395 CCAAAA 400
Db 326 TGA AAA 331
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RESULT 15
US-10-178-449A-15
; Sequence 15, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 439
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; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 276, 288, 349, 438
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-15

Query Match      31.0%; Score 138.4; DB 15; Length 439;
Best Local Similarity 71.9%; Pred. No. 2.8e-28;
Matches 192; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

Qy 155 AGATATCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAGACATGTCGGGAAA 214
Db 93 AGAAATCGGATCGGTGAAGGAGAACTATGTGAGAGGCAAGCAAGACATGTCGTGAAA 152

Qy 215 CTGTGGCAATACGGGACATTTGTGACAACTTAAATCATGGGAGGGTGGGCCCATGG 274
Db 153 TTGTGTTAAACACAGACATTTGTGACCAATGCAAGTCTTGGGAGGGTGCAGCCCATGG 212

Qy 275 AGCGTGTGTCATGTGCTTAACGGGAAACACATGTGTTTCTGTTACTTCAATTGTAAAAAGC 334
Db 213 AGCTTGTGTCATGTGCGCGGTGGGAAACACATGTGCTTCTGCTACTTCCAGTGCCTCAAGC 272

Qy 335 CGAAAAGCTTCTCAA -GACAAACTTAAAGCCGAACTCGCTCAAGCAAACTTAATG 393
Db 273 CGAAGAAGATGCCCGGATTAACCTCCGAGCTGAAGAGCTTGCCCAAGGAGAGATTGA 332

Qy 394 CCAAAAAGCTTGACCGTGTGATGCCAAGA 420
Db 333 GCTGAAAAGAGCCAGNCACCTTGA 359
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Search completed: March 18, 2005, 19:33:33
Job time : 422 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2005, 12:39:02 ; Search time 7103 Seconds
(without alignment)
2390.070 Million cell updates/sec

Title: US-09-763-019-5
Perfect score: 446
Sequence: 1 atggtgaatcggtcggttcg.....ttccaaacgttgaaacatccg 446

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gssi:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198.6	44.5	604	5	BQ989575 QGF18A17.
2	197	44.2	616	5	BQ984300 QGE21E24.
3	197	44.2	620	5	BQ984745 QGE4h04.Y
4	197	44.2	641	5	BU008575 QGH7P24.Y
5	177.2	39.7	547	1	BQ995419 QGF9P04.Y
6	160.6	36.0	468	1	AJ412176 AJ412176
7	154.2	34.6	606	6	CD846862 DH0AB512E
8	153.6	34.4	475	1	AJ541276 AJ541276
9	131.2	29.4	239	5	BQ844100 QGA12M13.
10	127	28.5	359	1	AJ541406 AJ541406
11	127	28.5	420	1	AJ541283 AJ541283
12	123.6	27.7	603	5	BQ847005 QGA20O20.
13	122	27.4	447	1	AJ306450 AJ306450
14	100.2	22.5	487	1	AJ412470 AJ412470
15	94	21.1	340	5	BQ845488 QGA16N20.
16	94	21.1	341	5	BQ861273 QGC18A12.
17	77.6	17.4	605	5	BU011479 QGJ16F16.
18	76	17.0	594	5	BU014657 QGJ7P01.Y
19	76	17.0	643	5	BU011346 QGJ15P15.
20	76	17.0	669	5	BQ990734 QGF20P11.
21	76	17.0	673	5	BU012409 QGJ1N15.Y
22	76	17.0	692	5	BQ999150 QGG21E06.
23	76	17.0	692	5	BU014714 QGJ8C12.Y
24	76	17.0	698	5	BQ990122 QGF19I14.

25	76	17.0	701	5	BQ988151
26	76	17.0	767	5	BU012833
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28	72.8	16.3	656	5	BU014798
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37	66.2	14.8	445	1	AV824429
38	62.6	14.0	363	7	CN847468
39	62.2	13.9	516	8	BH581774
40	60.4	13.5	673	8	BH657225
c 41	53	11.9	918	9	CL504812
42	52	11.7	371	7	C0749420
c 43	51.6	11.6	721	8	BH473290
44	45.8	11.2	379	7	CF270036
45	48.6	10.9	394	4	BG321454

ALIGNMENTS

RESULT 1
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LOCUS BQ989575 604 bp mRNA linear EST 21-AUG-2002
DEFINITION QGF18A17.YG.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
QGF18A17, mRNA sequence.
ACCESSION BQ989575
VERSION BQ989575.1 GI:22409110
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
REFERENCE 1 (bases 1 to 604)
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riaseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
JOURNAL Unpublished (2002)
COMMENT Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig6866, see http://cgdb.ucdavis.edu/
for details.
Plate: QGF18 row: A column: 17.

FEATURES
source
Location/Qualifiers
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/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="L.serriola"
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/clones="QGF18A17"
/lab_host="E.coli"
/clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRCDNAS1AB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and

transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>
TAG_TISSUE=germinating seeds
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=TCTGTGCGGG

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ORIGIN
Query Match      44.5%; Score 198.6; DB 5; Length 604;
Best Local Similarity 82.0%; Pred. No. 7.5e-43;
Matches 242; Conservative 0; Mismatches 49; Indels 4; Gaps 1;

Qy 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGGTCGGGAAA 214
Db 106 AGATATCACGAGTGTGAGAGGAGAACTATGCGAGAAACCTAGCAAGACATGGTCGGGTAA 165

Qy 215 CTGTGGCAATACGGGACATTTGTGACACCAATGTAATCATGGAGGGTGGGCCCATGG 274
Db 166 CTGTGGCAACACCGGACATCTGTATGGCCAGTGCANAATCTTTGGAGGGTGGAGCCCATGG 225

Qy 275 AGCGTGTCTATGCGGTAAACGGGAAACACATCTGTTTCTGTTTACTTCAATTGTAATAAAGC 334
Db 226 AGCATGTCACTGCTGGTGGAGGAAACACATCTGTTTCTGTTTACTTCAATTGTTCTTAAGC 285

Qy 335 CGAAAGCTTCTCAAGACAAACTTAAAGCCGAAACAACTCGCTCAAGACAAACTTAAATGC 394
Db 286 TGAAGAAGCTTCCCAAGACAAACTCAAAAGCCGAAAGAGCTCGCTCAAGACAAACTCAAAGC 345

Qy 395 CCRAAGCTTGACCG----TGATGCCAAGAAAGTGTTCRAAAGCTTGAACATCC 445
Db 346 TAAAGAAGCTAGACCGGCATGAGGACAAAGAAAGTAGTACCAAAATGTGGACCATCC 400
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LOCUS      BQ984300
DEFINITION BQ984300.616 bp mRNA linear EST 21-AUG-2002
            QGE21E24.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGE21E24, mRNA sequence.
ACCESSION  BQ984300
VERSION    BQ984300.1 GI:22401825
KEYWORDS   EST.
SOURCE     Lactuca sativa
            Lactuca sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
            Cichorieae; Lactuca.
            1 (bases 1 to 616)
            Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riesberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
            Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
            Lai,Z., Church,S., Jackson,L. and Bradford,K.
            Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
            Unpublished (2002)
            Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Amundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig6866, see http://cgdb.ucdavis.edu/
            for details.
            Plate: QGE21 row: E column: 24.
            Location/Qualifiers
                1..616
                /organism="Lactuca sativa"
                /mol_type="mRNA"
                /cultiivar="L.serriola"
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                /lab_host="E.coli"
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FEATURES
source

/clone lib="QG_EFGHJ lettuce serriola"
/note=Vector: pBRCNDSFIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>
TAG_TISSUE=germinating seeds
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=TCTGTGCGGG

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ORIGIN
Query Match      44.2%; Score 197; DB 5; Length 616;
Best Local Similarity 81.7%; Pred. No. 2e-42;
Matches 241; Conservative 0; Mismatches 50; Indels 4; Gaps 1;

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Db 106 AGATATCACGAGTGTGAGAGGAGAACTATGCGAGAAACCTAGCAAGACATGGTCGGGTAA 165

Qy 215 CTGTGGCAATACGGGACATTTGTGACACCAATGTAATCATGGAGGGTGGGCCCATGG 274
Db 166 CTGTGGCAACACCGGACATCTGTATGGCCAGTGCANAATCTTTGGAGGGTGGAGCCCATGG 225

Qy 275 AGCGTGTCTATGCGGTAAACGGGAAACACATCTGTTTCTGTTTACTTCAATTGTAATAAAGC 334
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Qy 335 CGAAAGCTTCTCAAGACAAACTTAAAGCCGAAACAACTCGCTCAAGACAAACTTAAATGC 394
Db 286 TGAAGAAGCTTCCCAAGACAAACTCAAAAGCCGAAAGAGCTCGCCCAAGACAAACTCAAAGC 345

Qy 395 CCRAAGCTTGACCG----TGATGCCAAGAAAGTGTTCRAAAGCTTGAACATCC 445
Db 346 TAAAGAAGCTAGACCGGCATGAGGACAAAGAAAGTAGTACCAAAATGTGGACCATCC 400
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LOCUS      BQ984745
DEFINITION BQ984745.620 bp mRNA linear EST 21-AUG-2002
            QGE4H04.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGE4H04, mRNA sequence.
ACCESSION  BQ984745
VERSION    BQ984745.1 GI:22402270
KEYWORDS   EST.
SOURCE     Lactuca sativa
            Lactuca sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
            Cichorieae; Lactuca.
            1 (bases 1 to 620)
            Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riesberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
            Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
            Lai,Z., Church,S., Jackson,L. and Bradford,K.
            Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
            Unpublished (2002)
            Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Amundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            belongs to contig QG_CA_Contig6866, see http://cgdb.ucdavis.edu/
            for details.
            Plate: QGE4 row: h column: 04.
            Location/Qualifiers
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FEATURES

JOURNAL
COMMENT

Unpublished (2002)
Contact: Alexander Kozik [R.W.Micheltmore]
Department of Vegetable Crops, R.W.Micheltmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [micheltmore@vegmil.ucdavis.edu]
belongs to contig QG_CA_Contig6866, see http://cgdb.ucdavis.edu/
for details.
Plate: QGF9 row: P column: 04.

FEATURES
source

Location/Qualifiers
1..547

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/note="Vector: pBRCDNASFIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgdb.ucdavis.edu/
TAG TISSUE=germinating seeds
TAG_LIB=QG_EFGHJ lettuce serriola
TAG_SEQ=TCTGTGCGGG"

ORIGIN

Query Match 39.7%; Score 177.2; DB 5; Length 547;

Best Local Similarity 82.6%; Pred. No. 4.6e-37; Indels 5; Gaps 2;
Matches 228; Conservative 0; Mismatches 43;

QY 174 GGAGAACTATCGGAAAGCTAGCAAGACATGGTGGGAAACTGTGGCAATACGGGACAT 233
DB 3 GGAGAACTATCGGAAACCTAGCAAGA-ATGGTCGGTAACTGTGGCAACACGGGAC 61
QY 234 TGTGACACCAATGTAATCATGGAGGGTGGGCCCATGGAGGTGTCATGTCGGTAAC 293
DB 62 TGTGATGCCAGTGCATAATCTTGGAGGGTGGGCCCATGGAGCATGTTCACGTGCGTGA 121
QY 294 GGGAAACACATGTGTTCTGTTACTTCAATTTGTAATAAGCGGAAAGCTTGTCTCAAGAC 353
DB 122 GGGAAACACATGTGTTCTGTTACTTCAATTTGTTAAAGCTGAAAGCTTGGCCCAAGAC 181
QY 354 AAACCTTAAGCGCAACAACTCGCTCAAGACAACTTAATGCCAAAGCTTGCACCG--- 409
DB 182 AAACCTCAAGCGCAAGAGCTCGCCCAAGACAACTCAAGCTTAATAAGCTAGACCGGCCA 241
QY 410 TGATGCCAAGAAAGTGGTTCACCAAGTTCACATCC 445
DB 242 TGAGCAAGAAGTAGTACCAAAATGTGGACCATCC 277

RESULT 6
AJ412176

LOCUS AJ412176 Helianthus annuus cv. Emil protoplast Helianthus annuus
DEFINITION cDNA clone HaDpIR101A04, mRNA sequence.

ACCESSION AJ412176

VERSION AJ412176.1 GI:15005431

KEYWORDS EST.

SOURCE Helianthus annuus (common sunflower)

ORGANISM Helianthus annuus

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.

REFERENCE
AUTHORS

Tamboirdeguy, C.; Ben, C.; Liboz, T. and Gentsbittel, L.
Sequence evaluation of four specific cDNA libraries for
developmental genomics of sunflower

JOURNAL

Mol. Genet. Genomics 271 (3), 367-375 (2004)

COMMENT

Contact: Gentsbittel L
Laboratoire de Biotechnologie et Amélioration des Plantes
Institut National Polytechnique de Toulouse - Ecole National
Supérieure Agronomique de Toulouse
IFR40, Pole de Biotechnologie Vegetale, 18 chemin de Borde Rouge,
Auzeville, CASTANET TOLOSAN 31326, France.

FEATURES
source

Location/Qualifiers
1..468
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="Emil"
/db_xref="taxon:4232"
/clone="HaDpIR101A04"
/cell_type="protoplast"
/clone_lib="Helianthus annuus cv. Emil protoplast"

ORIGIN

Query Match 36.0%; Score 160.6; DB 1; Length 468;

Best Local Similarity 78.1%; Pred. No. 1.4e-32;
Matches 193; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATCGGAAAGCTAGCAAGACATGGTCCGGAAA 214
DB 94 AGAAATCGGATCGGTGAAGGAGAAATATGTGAGAGGCAAGCAAGACATGGTCCGGAAA 153
QY 215 CTGTGCAATACGGGACATTTGTGACACCAATGTAATCATGGAGGGTGGGCCCATGG 274
DB 154 ATGTGGCAACACAAGACACTGTGATGACCAAGTCTTGGAGGGTGGAGCCCATGG 213
QY 275 AGCGTGTGATGTCGTTAAACCGGAAACACATGTGTTCTGTACTTCAATTTGTAATAAGC 334
DB 214 AGCTTGTGATGTCGCGGTGGGAAACACATGTGTTCTGTACTTCAACTGTTCCAAAGC 273
QY 335 CGAAAGCTTGTCTCAAGACAACTTAAAGCCGAAACACTCGCTCAAGACAACTTAATGC 394
DB 274 CCAGAGTTGGCTCAGGATTAACCTCAGACGAGAGAGCTCGCCCAAGGAGAGATTGAAGC 333
QY 395 CCAAAAG 401
DB 334 CGAAAG 340

RESULT 7

CD846862

LOCUS DHOAB512E07RM1 HaDevR1 Helianthus annuus cDNA clone HaDevR151E07,

DEFINITION mRNA sequence.

ACCESSION CD846862

VERSION CD846862.1 GI:32530694

KEYWORDS EST.

SOURCE Helianthus annuus (common sunflower)

ORGANISM Helianthus annuus

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; campanulids; Asterales; Asteraceae; Asteroideae;

Heliantheae; Helianthus.

1 (bases 1 to 606)

Genoplatte.

Genoplatte, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (http://www.genoplatte.com

and http://genoplatte-info.infobiogen.fr).

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FEATURES
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      1..606
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        /cultivar="psc8"
        /db_xref="taxon:4232"
        /clone="HadevR151807"
        /tissue_type="leaves"
        /clone_lib="HadevR1"

ORIGIN
  Query Match      34.6%; Score 154.2; DB 6; Length 606;
  Best Local Similarity 76.5%; Pred. No. 8e-31;
  Matches 189; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 155 AGATATCGCATCGGTAGTGGAGAACTATGCGAGAAAGCTACGAAGACATGTCGCGGAAA 214
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Db 97 AGAATTCGGATCGGTGAAAGGAGAAATTTATGTGAGAGGCGAAGCCAGACATGTCGCGGAA 156
      |||||
QY 215 CTGTGGCATACGGACATGTCACACCAATGTAATCATCGGAGGGTGCAGCCCATGG 274
      |||||
Db 157 ATGTGGCAAGACAAAACACTGTGATGACCAAGTCTTGGGAGGGTGCAGCCCATGG 216
      |||||
QY 275 ACGGTGTATGTGCGTAAACGGGAAACACATGTTTCTGTTACTTCAATTTGAAAAAGC 334
      |||||
Db 217 ACTTGTCTACGTGCGGATGGGAAACACATGTTCTGCTACTTCAACTGTTCCAAAGC 276
      |||||
QY 335 CGAAAGCTTGTCTAAGCAAACTTTAAAGCCGAAACACTCGCTCAAGACAAACTTAATGC 394
      |||||
Db 277 CCAGAAAGTTGGCTCAGGATAAATCAGAGCGGAGAGCTCGCCAGGAGAGATTGAACC 336
      |||||
QY 395 CCAAAAG 401
      |||||
Db 337 CGAAAAG 343

RESULT 8
AJ541276
LOCUS AJ541276 HaDpR1 Helianthus annuus cDNA clone HO0003K05, mRNA
DEFINITION
ACCESSION AJ541276
VERSION AJ541276.1 GI:28370751
KEYWORDS
SOURCE Helianthus annuus (common sunflower)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; campanulids; Asterales; Asteraceae; Asteroideae;
  Heliantheae; Helianthus.
REFERENCE
  1 (bases 1 to 475)
  Tamborindéguy, C., Ben, C., Liboz, T. and Gentsbittel, L.
  Sequence evaluation of four specific cDNA libraries for
  developmental genomics of sunflower
  Mol. Genet. Genomics 271 (3), 367-375 (2004)
JOURNAL
  Contact: Tamborindéguy C
  Laboratoire de Biotechnologie et Amélioration des Plantes
  Institut National Polytechnique de Toulouse - Ecole National
  Supérieure Agronomique de Toulouse
  IFRA40, Pole de Biotechnologie Végétale, 18 chemin de Borde Rouge,
  Auzeville, CASTANET TOLOSAN 31326, France.
FEATURES
  source
    Location/Qualifiers
      1..475
        /organism="Helianthus annuus"
        /mol_type="mRNA"
        /cultivar="Emil"
        /db_xref="taxon:4232"
        /clone="HO0003K05"
        /tissue_type="hypocotyl"
        /cell_type="protoplast"
        /dev_stage="1- to 5-days old protoplast"
        /clone_lib="HadevR1"

ORIGIN
  Query Match      34.4%; Score 153.6; DB 1; Length 475;
  Best Local Similarity 77.5%; Pred. No. 1.1e-30;
  Matches 186; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 162 GCATCCGTTAGTGGAGAACTATGCGAGAAAGCTACGAAGACATGTCGCGGAAACTGTGCG 221
      |||||
Db 4 GATCGGTGAAGGAGAAATTTATGTGAGAGGCGAAGCAAGACATGTCGCGGAAATGTGCG 63
      |||||
QY 222 AATACGGGACATTTGTGACAAACCAATGTAAATCATGGAGGGTGCAGCCCATGAGCGTGT 281
      |||||
Db 64 AACACAGACACTGTGATGACCAAGTGCAGTCTTGGAGGGTGCAGCCCATGAGCTTGT 123
      |||||
QY 282 CATGTGCGTAACGGGAAACACATGTTTCTGTTACTTCAATTTGAAAAAGCCGAAAG 341
      |||||
Db 124 CATGTGCGCGGTGGGAAACACATTTGTGCTTCTGCTACTTCAACTGTTTCAAAAGCCGAGAG 183
      |||||
QY 342 CTTGCTCAAGACAAACTTTAAAGCCGAAACAACTCGCTCAAGACAAACTTTAATGCCCAAAAG 401
      |||||
Db 184 TTGGCTCAGGATTAACCTCAGAGCAGAGAGCTGCGCAAGGAGAGATTTGAAGCCGAAAG 243
      |||||

RESULT 9
BQ844100
LOCUS BQ844100
DEFINITION BQ844100.1 GI:22224503
ACCESSION BQ844100
VERSION BQ844100.1
KEYWORDS
SOURCE Lactuca sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
  Cichorieae; Lactuca.
REFERENCE
  1 (bases 1 to 239)
  Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
  Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
  Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
  Lai, Z., Church, S., Jackson, L. and Bradford, K.
  Lettuce and Sunflower ESTs from the Compositae Genome Project
  http://compgenomics.ucdavis.edu/
  Unpublished (2002)
JOURNAL
  Contact: Alexander Kozik [R.W.Michelmore]
  Department of Vegetable Crops, R.W.Michelmore Lab
  University of California at Davis (UCD)
  Asmumson Hall, UCD, Davis, CA 95616, USA
  Tel: 1-(530)-742-1742
  Fax: 1-(530)-752-9659
  Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
  belongs to contig QG_CA_Contig6866, see http://cgdb.ucdavis.edu/
  for details.
  Plate: QGAl2 row: M column: 13.
FEATURES
  source
    Location/Qualifiers
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        /organism="Lactuca sativa"
        /mol_type="mRNA"
        /cultivar="Salinas"
        /db_xref="taxon:4236"
        /clone="QGAl2M13"
        /lab_host="E.coli"
        /clone_lib="QG ABCDI lettuce salinas"
        /note="Vector: pBRCDNASFIAB; The library was constructed
        from 10 different sources of RNA from a single genotype.
        Separate cDNAs were generated using primers that
        incorporated unique 5' and 3' tags to distinguish each
        source of RNA. cDNAs were then pooled, size-fractionated,
        directionally cloned into a custom medium-copy vector and
        transformations made with four size classes to minimize
        size bias. Details of each source of RNA and library
        construction can be obtained at http://cgdb.ucdavis.edu/
        TAG_SEQ=Not found"

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ORIGIN

Query Match	29.4%	Score 131.2;	DB 5;	Length 239;
Best Local Similarity	81.4%;	Pred. No. 1.2e-24;		
Matches 162;	Conservative 0;	Mismatches 36;	Indels 1;	Gaps 1;
QY	155	AGATATCCATCCGTTAGTGGAGAACTATCGGAGAAAGCTAGCAGACACATGTCGGGAAA	214	
Db	41	AAATATCACGAGTGTGAGAGAGAACTATCGGAGAAANCTAGNAAAGAAATGTCGGGTAA	100	
QY	215	CTGTGGCAATACGGGACATTTGTGACACCAATGTAAATCATGGAGGGTGGCGGCCATGG	274	
Db	101	CTGTGGAACACCGGACACATGTGATGSCCAGTSCAAATCTTGGAGGGTGGAGGCCATGG	160	
QY	275	AGCGTGTCATGTCGGTAAACGGGAAACACATGTGTTCTGTACTTCAATGTG-AAAAAG	333	
Db	161	AGCATGTACATGTCGCTGGAGGGAACACATGTGCTTCTGCTACTTTAAATTGTCCTAAAG	220	
QY	334	CCGAAAAGCTTGTCTCAAGA	352	
Db	221	CTGAAAAGCTTTGCCAAGA	239	

RESULT 10	AJ541406	359 bp	mrna	linear	EST 04-MAY-2004
LOCUS	AJ541406				
DEFINITION	AJ541406	HaDp8r1	Helianthus annuus	cDNA clone	HO0005105, mRNA
ACCESSION	AJ541406				
VERSION	AJ541406.1	GI:28370881			
KEYWORDS	EST.				
SOURCE	Helianthus annuus			(common sunflower)	
ORGANISM	Helianthus annuus				

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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FEATURES
source
Location/Qualifiers
1. .359
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="Emil"
/db_xref="taxon:4232"
/clone="HO0005105"
/tissue_type="hypocotyl"
/cell_type="protoplast"
/dev_stage="1- to 5-days old protoplast"
/clone_lib="HabosR1"

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Query Match	28.5%	Score 127;	DB 1;	Length 359;
Best Local Similarity	77.4%	Prod. 1.7e-23;		
Matches 154;	Conservative	0; Mismatches	45; Indels	0; Gaps
205	GGTGGGAACTGTGGCAATACGGGACATTTGGACAACCAATGTAAATCATGGGAGGTG	264		
4	GGTCCGGAAATGTGGCAACACAAGACACACTGTGGACGACCGAGTGCAGTCTTTGGGAGGTG	63		

265 CGCCCATGAGCGTGCATGTGGTAACGGGAACACATGTTCTGTCTCAATT 324
64 CAGCCCATGAGCTGTGCAGTGGCGGTGGGAACACATGTTCTGTCTCAACT 123

325 GTAAAAGCGGAAAGCTTGTCTCAAGACAAACTTAAAGCCGAACACTCGCTCAAGACA 384
Qy |||||
124 GTTCCAAAGCCGAGAAGTGTGGCTCAGGATAAACTTCATAGCAGAAGAGCTGCGCAAGGAGA 183
Db |||||
385 AACTTAATGCCCAAAAGCT 403
Qy |||||
184 AGATTGAAGCCGAAAAGGT 202
Db |||||

RESULT 11
AJ541283

LOCUS	AJ541283	420 bp	mRNA	linear	EST 04-MAY-2004
DEFINITION	AJ541283	HapDer1	<i>Helianthus annuus</i>	CDNA clone	H00003K21, mRNA
ACCESSION	AJ541283				
VERSION	AJ541283.1	GI:28370758			
KEYWORDS	EST;				
SOURCE	<i>Helianthus annuus</i>	(common sunflower)			
ORGANISM	<i>Helianthus annuus</i>				

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
-------------------------------	--------------------

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
-------------------------------	--------------------

FEATURES
source

FEATURES
source

ORIGIN

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Query Match      28.5%; Score 127; DB 1; Length 420;
Best Local Similarity 77.4%; Pred. No. 1.8e-23;
Matches 154; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
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205	GGTCGGGAACTGTGTGCAATACGGGACATTGTGCAACCAATGTAAATCATGGGAGG	264	
	4	GGTCGGGAAATGTGGCAACAACAGACACTGTGACGACAGTCAAGTCTTGGGAGG	63
265	CGGCCCATCGAGCGTGTCAATGTGCGCTAACGGGAAACACATGTGTTCTGTACTTCAAT	324	
64	CAGCCCATCGAGCTGTGTCACGTGCGCGGTGGGAAACACATGTGTTCTGTACTTCAAT	123	

325 GTAAAAAAGCCGAAAGCTTGCTCAAGACAAACTTAAAGCGGAACAATCGCTCAAGACA 384
| | | | |
124 GTTCAAAGCCGAGAAGTTGGCTCAGGATAAACTCATAGCAGAAGAGCTCGCCAAGGAGA 183
| | | | |
385 AACTTAATGCCCAAAAGCT 403
| | | | |
184 AGATTGAAGCCGAAAAGGT 202
| | | | |

RESULT 12

Accession	Gene	Size	Type	Source	Accession
Q847005	OCUS	603 bp	mRNA	linear	EST 14-AUG-2002
Q847005	DEFINITION	QGA20020.yg.ab1	QGA20020	QGA20020	QGA20020
					QGA20020, mRNA sequence.


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ACCESSION   BQ847005
VERSION     BQ847005.1  GI:22230770
KEYWORDS    EST.
SOURCE      Lactuca sativa
ORGANISM    Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
            Cichorieae; Lactuca.
REFERENCE   1 (bases 1 to 603)
AUTHORS    Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
            Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
            Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
            Lai, Z., Church, S., Jackson, B. and Bradford, K.
            Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
            Unpublished (2002)
JOURNAL     Contact: Alexander Kozik [R.W.Michelmore]
COMMENT     Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundo Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozikeatgc.org [michelmore@vegmil.ucdavis.edu]
            belongs to contig QG_CA_Contig6866, see http://cgpdb.ucdavis.edu/
            for details.
            Plate: QGA20 row: O column: 20.
FEATURES    Location/Qualifiers
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                /clone_lib="QG ABCDI lettuce salinas"
                /note="Vector: pBRCNDASfiAB; The library was constructed
                from 10 different sources of RNA from a single genotype.
                Separate cDNAs were generated using primers that
                incorporated unique 5' and 3' tags to distinguish each
                source of RNA. cDNAs were then pooled, size-fractionated,
                directionally cloned into a custom medium-copy vector and
                transformations made with four size classes to minimize
                size bias. Details of each source of RNA and library
                construction can be obtained at http://cgpdb.ucdavis.edu/
                TAG TISSUE=germinating seeds
                TAG_LIB=QG ABCDI lettuce salinas
                TAG_SEQ=TCCTGTGCGGG"
ORIGIN
Query Match      27.7%; Score 123.6; DB 5; Length 603;
Best Local Similarity 71.8%; Pred. No. 1.6e-22;
Matches 204; Conservative 0; Mismatches 74; Indels 6; Gaps 3;
QY 168 GTTAGTGGAGACTATGCGAGAAAGCTAGCAAGACATGTCGGGAACTGGCAATAGC 227
DB 121 GTGATAGGAGAACTATGTGAGAAACCTACTGGGACTGGACCGCTAACATGTGTGAACACC 180
QY 228 GGACATTTGTGACAAACAAATGTAATCATGGAGGGTGGCGGCCCATGGAGCGTGTATGTG 287
DB 181 GGACACTGAGTGGTCAATCTTGTGAGGGTGTAGCCCTGGAGCATGTGCTTG 240
QY 288 CGTAACGGGAA-ACACATGTGTTTCTG-TTACTTCAATTGTAAAAAGCCGAAAAGCTTG 345
DB 241 CGTGGAGGGAAGACACGTCGAGCTTCTGCGTACTTTTATTGTCTTAAAGCTGAAGACTTG 300
QY 346 CTCAGACAACTTAAAGCCGAACAACTCGCTCAAGACAAACTTAATGCCCAAAAGCTTG 405
DB 301 CCCTTGACTGACTCAGAGCCAAAGAGCTCGCCCAAGACAACTCAAAGCTTAAAGAGCTAG 360
QY 406 ACCG---TGATGCCAAGAAAGTGGTCCAAACGTTGAACATCC 445
DB 361 ACCGGCCATGAGACAAAGAAAGTAGTACCATAATGTGGACCATCC 404

RESULT 13
LOCUS      AU306450
DEFINITION AU306450 zinnia cultured mesophyll cell equalized cDNA Zinnia
            elegans cDNA clone Z16034, mRNA sequence.
ACCESSION  AU306450
VERSION    AU306450.1  GI:41122386
KEYWORDS   EST.
SOURCE     Zinnia elegans
ORGANISM   Zinnia elegans
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; campanulids; Asterales; Asteraceae; Asteroideae;
            Heliantheae; Zinnia.
REFERENCE   1 (bases 1 to 447)
AUTHORS    Demura, T., Tashiro, G., Horiguchi, G., Kishimoto, N., Kubo, M.,
            Matsuoka, N., Minami, A., Nagata-Hiwatashi, M., Nakamura, K.,
            Okamura, Y., Sasea, N., Suzuki, S., Yazaki, J., Kikuchi, S. and
            Fukuda, H.
            Visualization by comprehensive microarray analysis of gene
            expression programs during transdifferentiation of mesophyll cells
            into xylem cells
            Proc. Natl. Acad. Sci. U.S.A. 99 (24), 15794-15799 (2002)
JOURNAL     Contact: Taku Demura
COMMENT     Morphogenesis Research Group
            RIKEN Plant Science Center
            1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9605
            Fax: 81-45-503-9573
            Email: demura@postman.riken.go.jp
            This clone was obtained at our laboratory
            Seq primer: M13 forward.
FEATURES    Location/Qualifiers
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                /clone_lib="zinnia cultured mesophyll cell equalized cDNA"
                /note="Vector: pGEM-T easy; cultured in tracheary element
                differentiation-inductive medium"
ORIGIN
Query Match      27.4%; Score 122; DB 1; Length 447;
Best Local Similarity 77.7%; Pred. No. 4e-22;
Matches 160; Conservative 0; Mismatches 45; Indels 1; Gaps 1;
QY 196 GCAAGACATGTCGGGAAACTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCAT 255
DB 1 GTAGACATGTCGGGAAATTTGTGCAACACAGACACTGCGATGCAGTCGCAAGTCCT 60
QY 256 GGGAGGGTGGCGGCCCATGAGCGTGTCAATGTCGTAACGGGAAACACATGTTTCTGTT 315
DB 61 GGGAGGGTGCAGCTCATGTTGTTTGTACGTCGCGGGTGGGAAACACATGTGCTTGTCT 120
QY 316 ACTTCAATTGTAAAAAGCCGAAAAGCTT-GCTCAAGACAACTTAAAGCCGAAACATC 374
DB 121 ACTTCAATTGTCAAAGCCGAGAGGTTGGCTCAGGATAAACTCAAAGCAGAAGAGCTC 180
QY 375 GCTCAAGACAAACTTAAATGCCCAAAA 400
DB 181 GCNAGGAGAGATTTGATGCTGGAAA 206

RESULT 14
LOCUS      AJ412470
DEFINITION AJ412470 Helianthus annuus cv. Email protoplast Helianthus annuus
            cDNA clone HapdIRI07C12, mRNA sequence.

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ACCESSION AJ412470
VERSION AJ412470.1 GI:15005725
KEYWORDS EST.
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          asterids; campanulids; Asterales; Asteraceae; Asteroideae;
          Heliantheae; Helianthus.
REFERENCE 1 (bases 1 to 487)
AUTHORS Tamboirdeguy,C., Ben,C., Liboz,T. and Gentzbittel,L.
TITLE Sequence evaluation of four specific cDNA libraries for
JOURNAL development genomic of sunflower
COMMENT Mol. Genet. Genomics 271 (3), 367-375 (2004)
Contact: Gentzbittel L
Laboratoire de Biotechnologie et Amelioration des Plantes
Institut National Polytechnique de Toulouse - Ecole National
Superieure Agronomique de Toulouse
IFR40, Pole de Biotechnologie Vegetale, 18 chemin de Borde Rouge,
Auzeville, CASTANET TOLOSAN 31326, France.
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    /cultivar="Emil"
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    /cell_type="protoplast"
    /clone_lib="Helianthus annuus cv. Emil protoplast"
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Query Match      22.5%; Score 100.2; DB 1; Length 487;
Best Local Similarity 65.6%; Pred. No. 3.3e-16;
Matches 162; Conservative 0; Mismatches 83; Indels 2; Gaps 1;
QY 155 AGATATCCATCCGTTAGTGGAGACTATGCGAGAACTGCGAGAACTAGCAAGACATGTCGGGAAA 214
Db 110 AGAAATCGGTAGCGGGAAGGAGATTATGTGAGAGGCAAGCAAGCAAGCGGAAA 169
QY 215 CTGTGGCAATACGGGACATTTGTACACCAATGTAAATCATGGAGGTTGGGCCCATGG 274
Db 170 AGGGGCAACACAGACATTTGTGGACCGGCAAGTTTAGGAGGTTGAGGCGCTTGG 229
QY 275 AGCGTGTATGTGCGTAAACGGGAACACATGTGTTTCTGTTTCTCAATTTGAAAAAGC 334
Db 230 AGTTGTTTATGTGCGCGGGGAAACACTTTTGTGTTTATGTAATTAATTAACAAAGC 289
QY 335 CGAAAGCTTCTCAAGACAACTTAAAGCCGACAACTCCCTCAAGACAACTTAATGC 394
Db 290 CCAGAG--TAGGTGAGTAAATACAGAGCAGAGAGTACGCCAAGGAGAAAGTTAGAAGC 347
QY 395 CCAAAAG 401
Db 348 CGAAAAAG 354
RESULT 15
BQ845488
LOCUS BQ845488
DEFINITION QGA16N20.YG.ab1 QG ABCDI lettuce salinas Lactuca sativa cDNA clone
ACCESSION BQ845488
VERSION BQ845488.1 GI:22227399
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
          Cichorieae; Lactuca.
REFERENCE 1 (bases 1 to 340)
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
          Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
          Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
          Lai,Z., Church,S., Jackson,L. and Bradford,K.
          Lettuce and Sunflower ESTs from the Compositae Genome Project
          http://compgenomics.ucdavis.edu/
          Unpublished (2002)
          Contact: Alexander Kozik [R.W.Michelmore]
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          Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
          belongs to contig QG_CA_Contig238, see http://cgpdb.ucdavis.edu/
          for details.
          Plate: QGA16 row: N column: 20.
          Location/Qualifiers
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             /clone="QGA16N20"
             /lab_host="E.coli"
             /clone_lib="QG ABCDI lettuce salinas"
             /note="Vector: pBRCNAsf1AB; The library was constructed
             from 10 different sources of RNA from a single genotype.
             Separate cDNAs were generated using primers that
             incorporated unique 5' and 3' tags to distinguish each
             source of RNA. cDNAs were then pooled, size-fractionated,
             directionally cloned into a custom medium-copy vector and
             transformations made with four size classes to minimize
             size bias. Details of each source of RNA and library
             construction can be obtained at http://cgpdb.ucdavis.edu/
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             TAG_LIB=QG ABCDI lettuce salinas
             TAG_SEQ=TGTAGCCGGG"
          Query Match      21.1%; Score 94; DB 5; Length 340;
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          Db 1 AGGGTGCAGCCCATGGAGCTTGCCACGTGGTGGAGGAAACACATGTGCTTCTGCTACT 60
          QY 319 TCAATTGTAATAAAGCCGAAAAGCTTGTCTCAAGACAAACTTAAAGCCGAACTCGCTC 378
          Db 61 TCAACTGTTTCAAAAAGCAGAGAAGATGGCTCAAGATAAGCTGAAAGCCAAAGAGCTCACCA 120
          QY 379 AAGACAAACTTAATGCCAAAAGCTTGACCGTGTATGCCAAGAAGTGGTTCCTCA 432
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